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(12) **United States Patent**  
**Oyadomari**(10) **Patent No.:** **US 9,085,791 B2**  
(45) **Date of Patent:** **Jul. 21, 2015**(54) **METHOD FOR SCREENING SUBSTANCE  
RELATING TO ENDOPLASMIC RETICULUM  
STRESS PARTICIPATING IN ONSET OF  
DIABETES**JP 2008-131899 A1 6/2008  
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TOKUSHIMA**, Tokushima-Shi (JP)(\*) Notice: Subject to any disclaimer, the term of this  
patent is extended or adjusted under 35  
U.S.C. 154(b) by 0 days.(21) Appl. No.: **13/983,864**(22) PCT Filed: **Feb. 6, 2012**(86) PCT No.: **PCT/JP2012/052650**

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(2), (4) Date: **Aug. 6, 2013**(87) PCT Pub. No.: **WO2012/108394**PCT Pub. Date: **Aug. 16, 2012**(65) **Prior Publication Data**

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(2013.01); **C12Y 104/03002** (2013.01); **G01N**  
**33/5008** (2013.01); **G01N 33/5076** (2013.01);  
**C07K 2319/60** (2013.01); **G01N 2333/4706**  
(2013.01); **G01N 2500/10** (2013.01); **G01N**  
**2800/042** (2013.01)(58) **Field of Classification Search**

None

See application file for complete search history.

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LLP(57) **ABSTRACT**A system for evaluating activation of the pathway mediated  
by ATF6. More specifically, a method for screening an endo-  
plasmic reticulum stressor, as well as a method for screening  
a substance for suppressing an endoplasmic reticulum stress  
induced by the activation of the pathway mediated by ATF6,  
and a method for screening an antidiabetic drug candidate. A  
method for real-time evaluation of activation of the pathway  
mediated by ATF6 in viable cells. The method uses a poly-  
nucleotide encoding a nonfluorescent peptide domain derived  
from a fluorescent protein and an ATF6 protein domain.**6 Claims, 14 Drawing Sheets**

FIG. 1

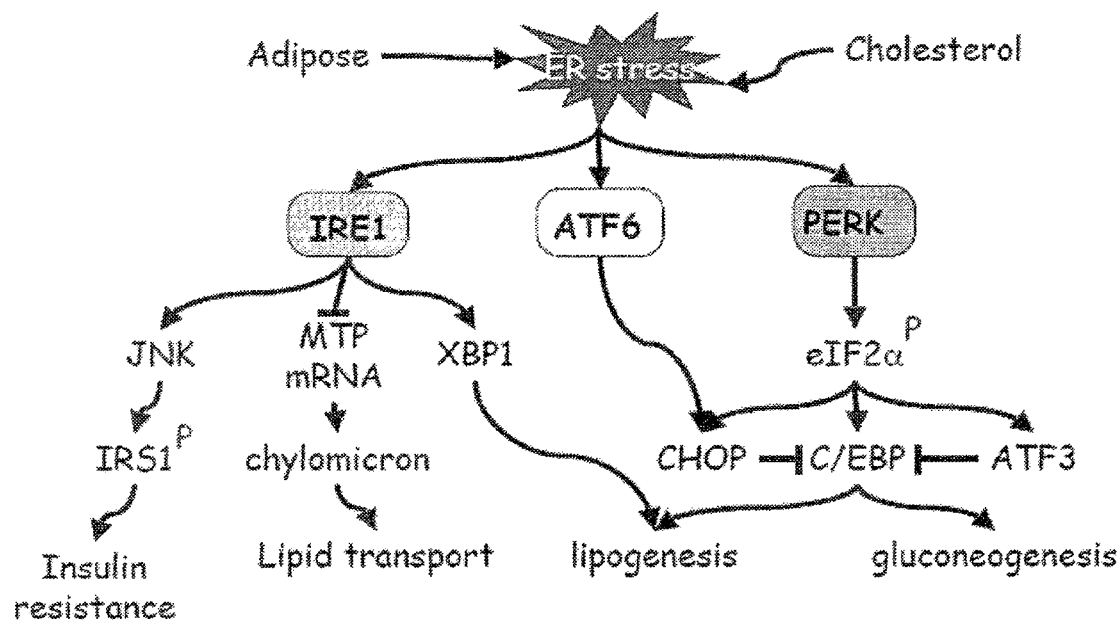


FIG. 2

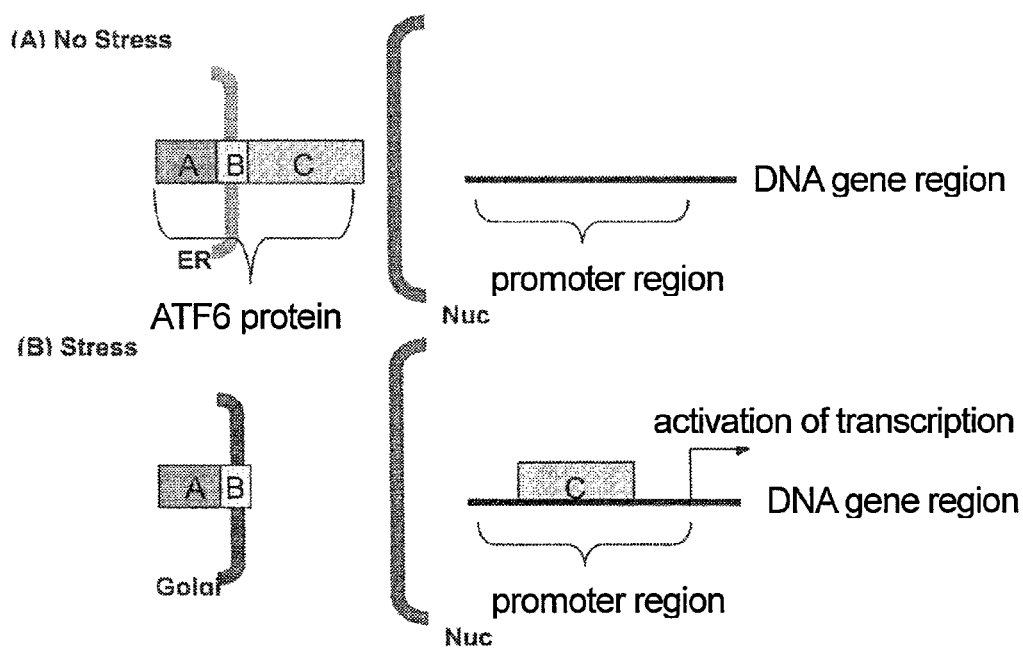


FIG. 3

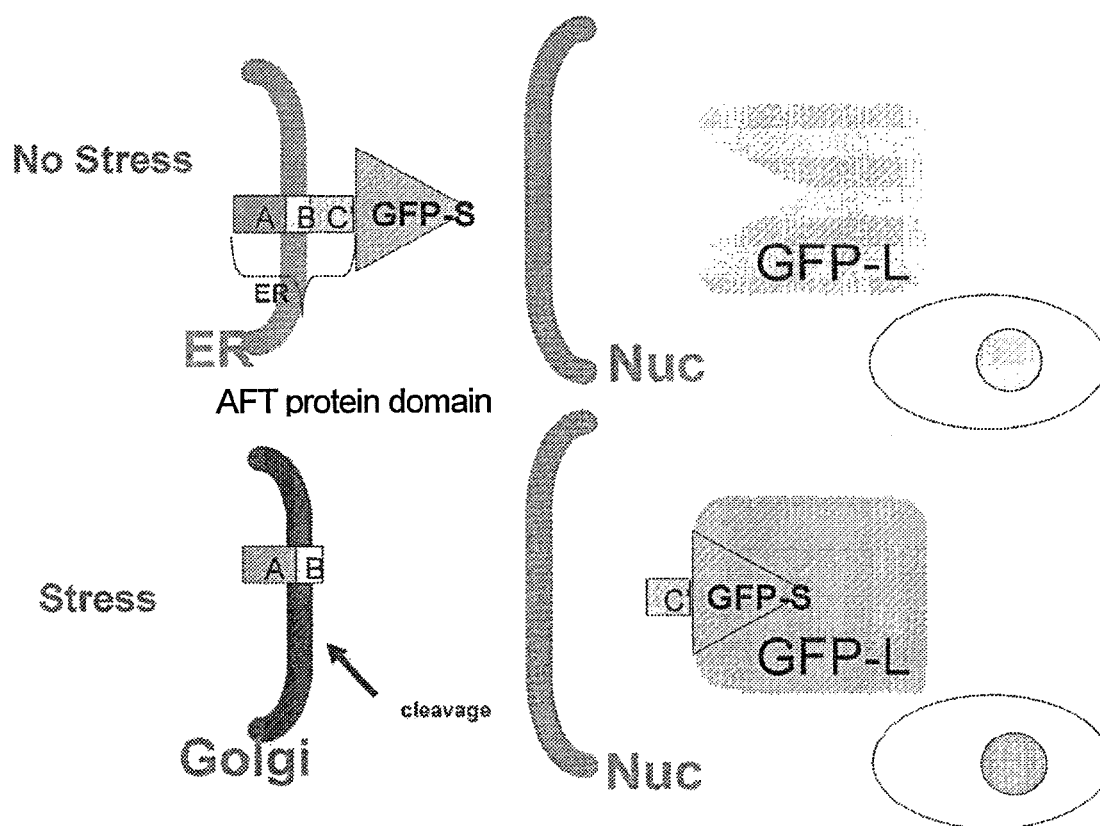


FIG. 4

EGFPS-ATF6d (Nhe1-Not1) (SEQ ID NO: 17)

CTAgccacc

ATGCGTGACCACATGGTCCTTCATGAGTACGTAAATGCTGCTGGGATTACA

Portion 1  
(SEQ ID NO: 18)

ggaggaggatccggagggtggcagc

Portion 2  
(SEQ ID NO: 19)GACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGACTACAAGGATGA  
CGATGACAAGPortion 3  
(SEQ ID NO: 20)

gatccaaaaagaagagaaaggtagatccaaaaagaagagaaaggtagatccaaaaagaagagaaaggta

Portion 4  
(SEQ ID NO: 21)

CTAGCGCTACCGGACTCAGATCTCGAG

agccatggcttccgcccggcgggtggcggcaggatgatggcacgctgccatgtcttggccaggagagcgggatggacc  
gtcacctgcagcctgtgcttctgctaggatcaatgtgPortion 5  
(SEQ ID NO: 22)

GGTACC

ccaaagcgaagagctgtctgtgtgatgatagtagcatttataatgctgaactatgggccatgagcatgctggagcaag  
aatcccgaagagtgaacctaagtgtgagccctccaatcagaggaggcatctcttgaatttcagcaaaagaagttaaag  
acacatcagatgggtgacaaccagaagacagttacagctatgatcactctgtgtccaatgacaagctttaatgggtgtaag  
tgaagagccattgctttatatgctccacctcatgtcaaccctgattaacacacagagtctctcaggtgaacctgaactt  
cgaggctgggttcatagacatgaagtggaaaggacaaatctagaagaatgacaaatagccaacagaaagcccgattct  
ccagggtgctctggaacagggtctaatctcagctgatggctgtccagtacacagaaaccactagcatcagtaggaattctg  
ggagtgagctgcaagtgtattacgctccctgggaagttaccaaggcttctttgacgcatccgaggaggaggagatacgttt  
tacgttgtctcatttgaagggtacatctgtctattaccagctaccaccacaacaagaccacaagacaaaaatgtcaattgt  
attaccagcaataaacataaatgataatgtgatcaatgggcaggactatgaagtaatgatgcagattgactgtcagggtgat  
ggacaccaggatctccacatcaaaagctcctcgggtccccccttatctccgggatcatcagcggaaaccaaacaccagcctctt  
tggttccctccaacaaccacagagacgacctgtggtcagcaccatccctgagtcgttgtagtagPortion 6  
(SEQ ID NO: 23)

GC

FIG. 5

EGFPL (NheI·NotI) (SEQ ID NO: 24)

ctaGCCACCATG

gatccaaaaagaagagaaaggtagatccaaaaagaagagaaaggtagatccaaaaagaagagaaaggta

Portion 7  
(SEQ ID NO: 25)

ATGGTGAGCAAGGGCGAGGAGCTGTTCAACGGGGTGGTGCCCATCCTGGTCGAGC  
TGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGagaGGCGAGGGCGAGGGCGA  
TGCCACCatcGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCC  
TGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTCAGCCG  
CTACCCCGACCACATGAAGaggCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT  
ACGTCCAGGAGCGCACCATCtctTTCAAGGACGACGGCaaaTACAAGACCCGCGCCgt  
aGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCactGACT  
TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACttAACAGCCAC  
AACGTCTATATCacgGCCGACAAGCAGAAGAACGGCATCAAGgctAACITCacagttCGC  
CACAAcgttGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCC  
CATCGGCGACGGCCCCGTGCTGCTGCCCCACAACCACTACCTGAGCACCCAGactgt  
cCTGAGCAAAGACCCCAACGAGAAgtaa

Portion 8  
(SEQ ID NO: 26)

agc

FIG. 9

DNA sequence in which only the spacer is changed to  
a sequence GGGS

TACGTAAATGCTGCTGGGATTACAGGAGGTGGCAGCGACTACAAAGACCATGACG  
GTGATTATAAAGATCATGACATCGACTACAAGGATGACGATGACAAGGATCCAAAA SEQ ID NO: 27  
AAGAAGAGAAAGGTAGATCCAAAAAAGAAGAGAAAGGTAGATCCAAAAAAGAAGA  
GAAAGGTACTAGCGCTACCGGACTCAGATCT

DNA sequence in which only the spacer is changed to  
a sequence GGS SGGG SGGG S

TACGTAAATGCTGCTGGGATTACAGGAGGAGGATCCGGAGGTGGCAGCGGAGGTG  
GCAGCGACTACAAAGACCATGACGGTGATTATAAAGATCATGACATCGACTACAAG  
GATGACGATGACAAGGATCCAAAAAAGAAGAGAAAGGTAGATCCAAAAAAGAAGA SEQ ID NO: 28  
GAAAGGTAGATCCAAAAAAGAAGAGAAAGGTACTAGCGCTACCGGACTCAGATCT

FIG. 6

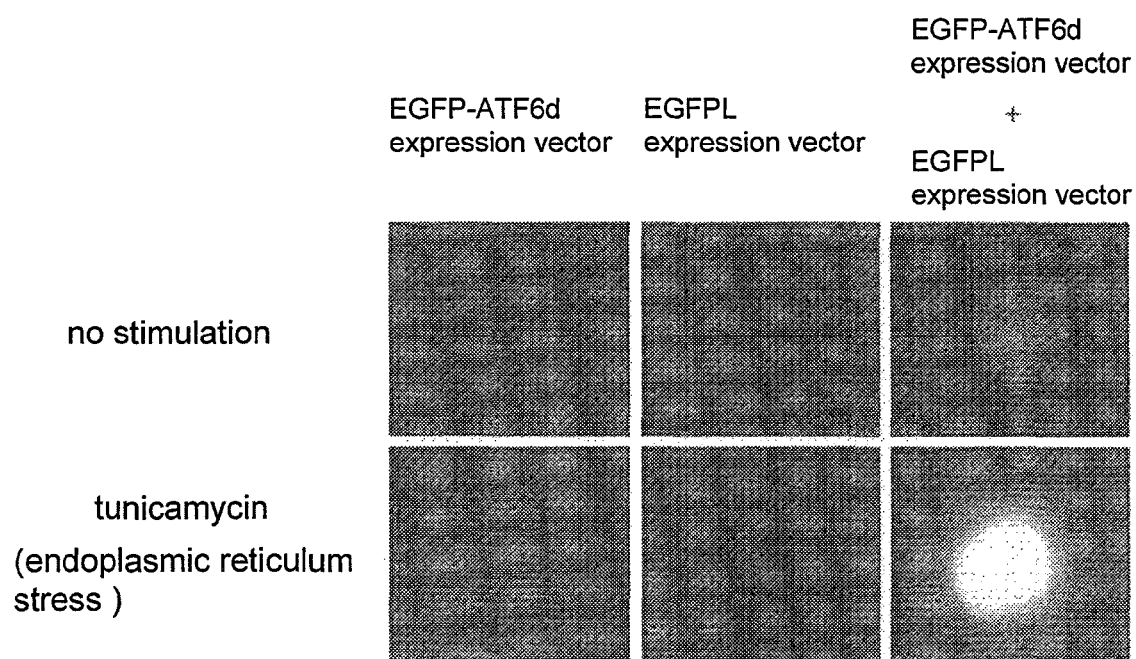


FIG. 7

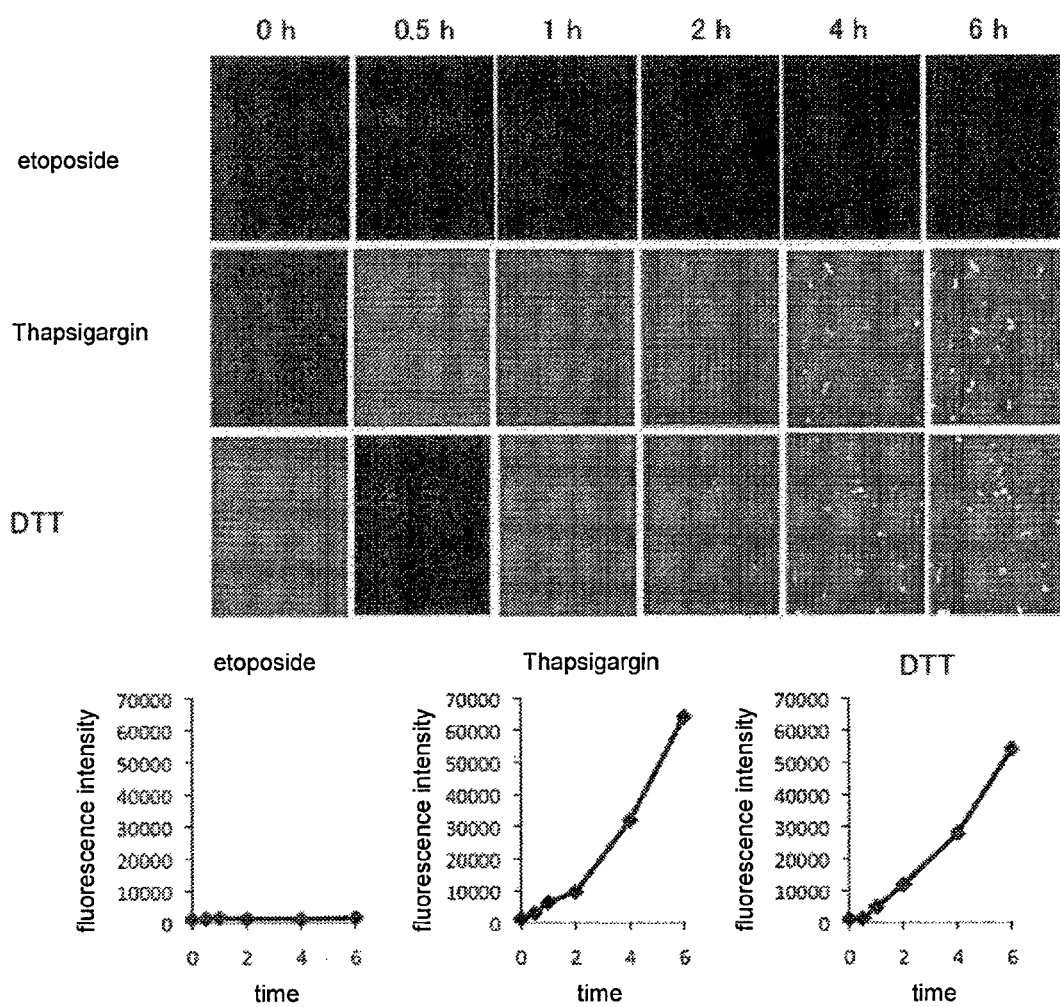


FIG. 8

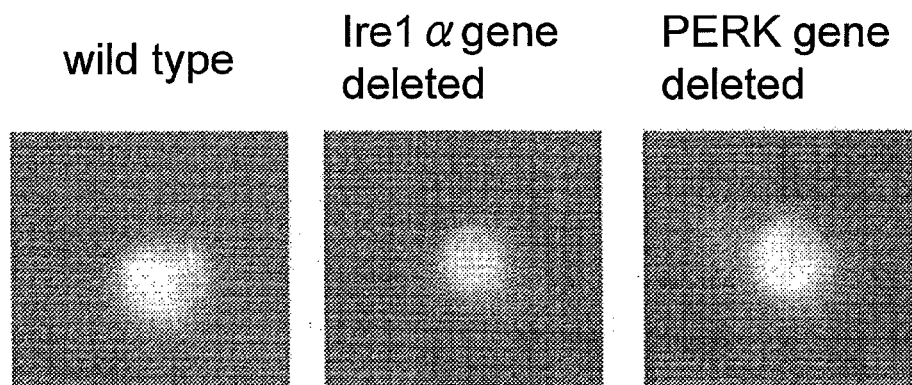


FIG. 10

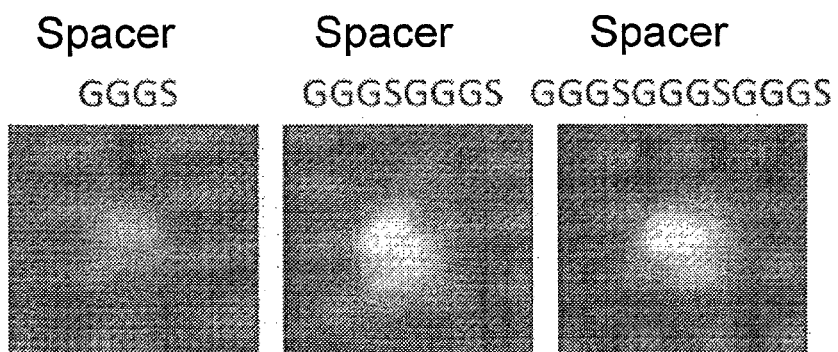




FIG. 11

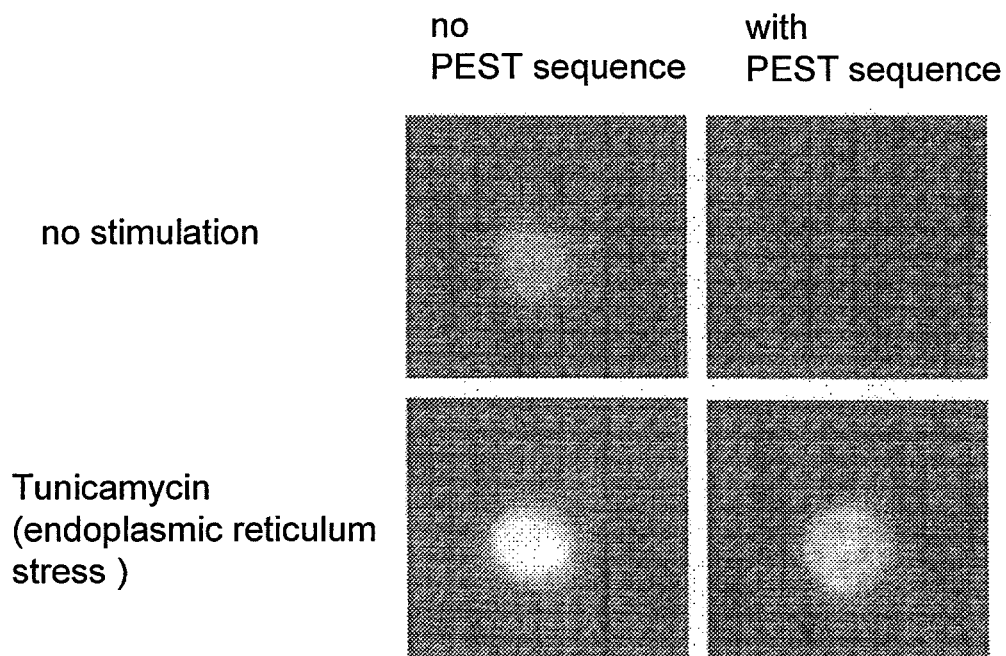


FIG. 12

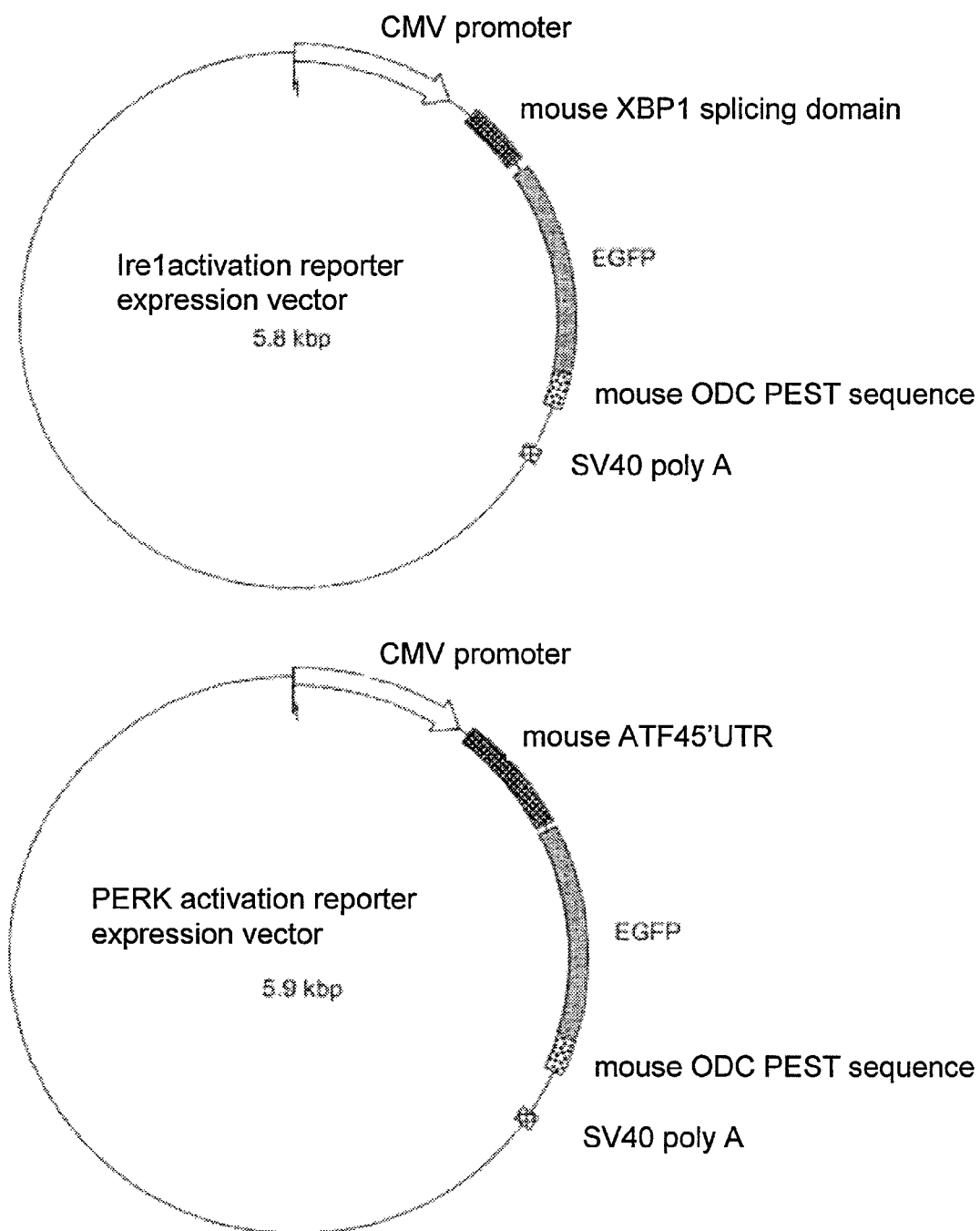


FIG. 13

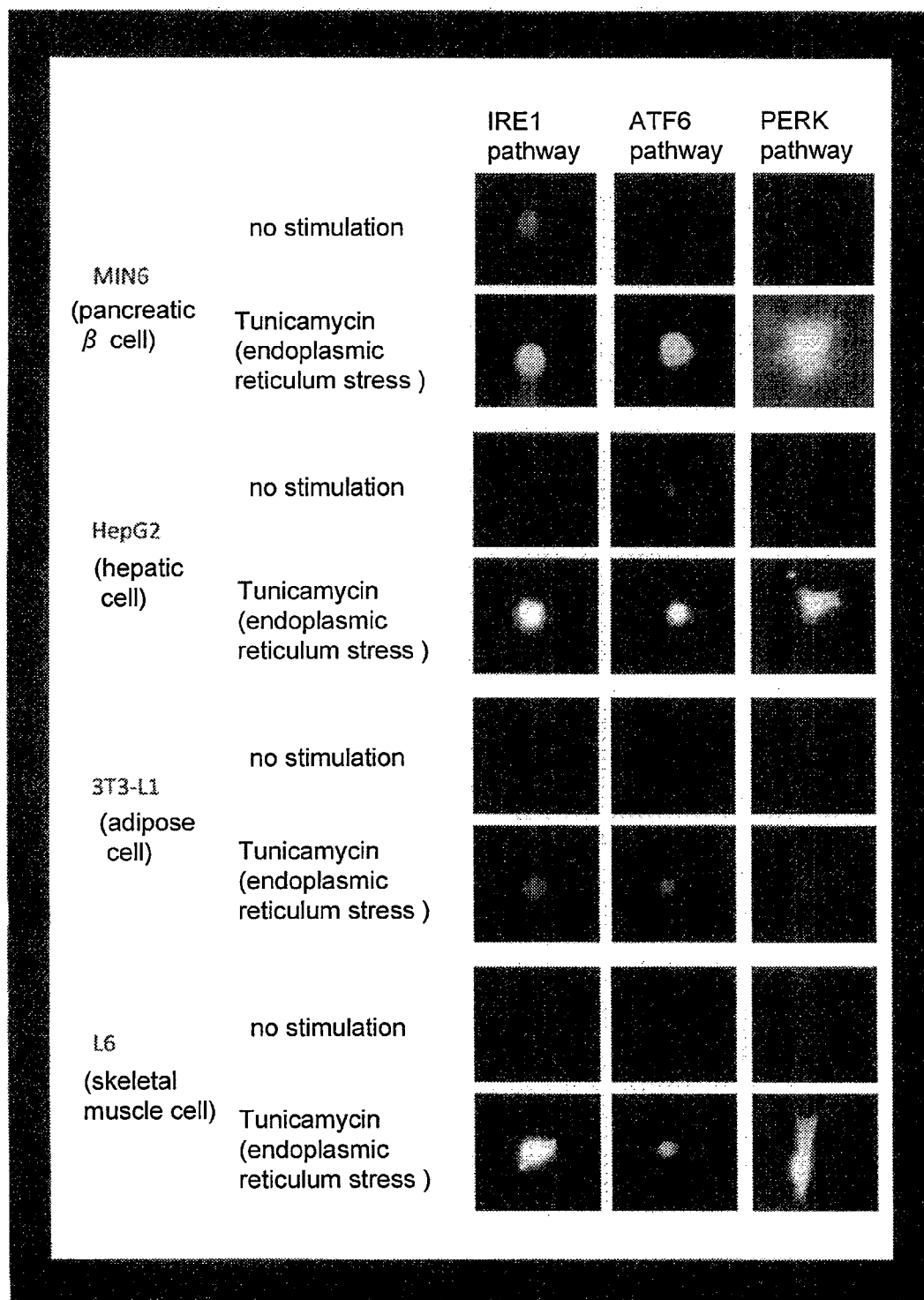


FIG. 14

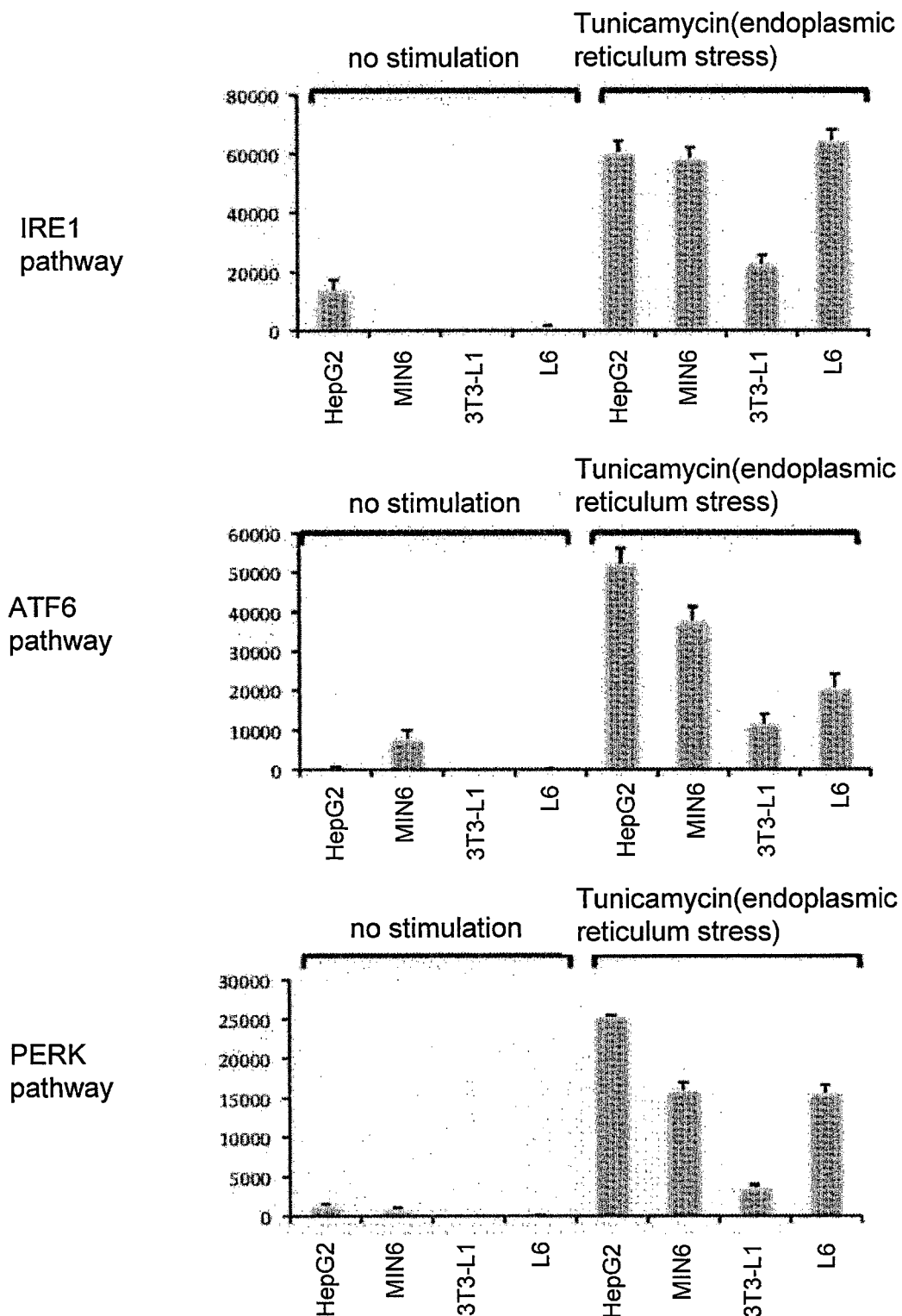


FIG. 15

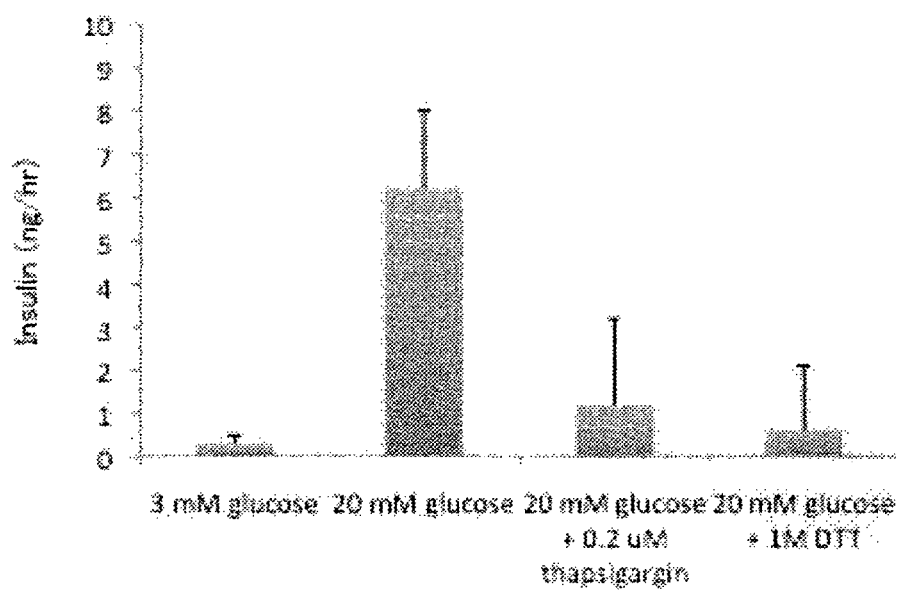


FIG. 16

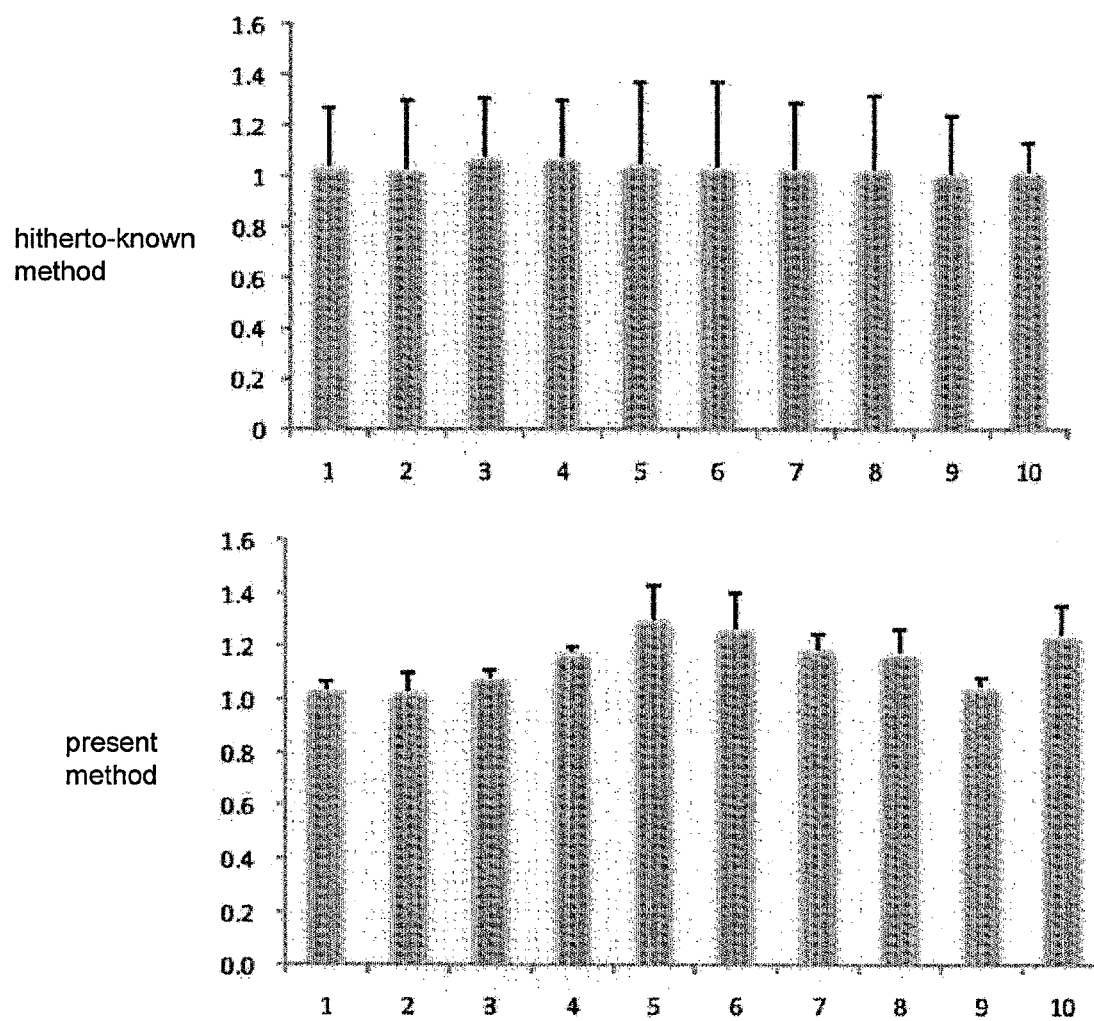


FIG. 17

## ERAI system

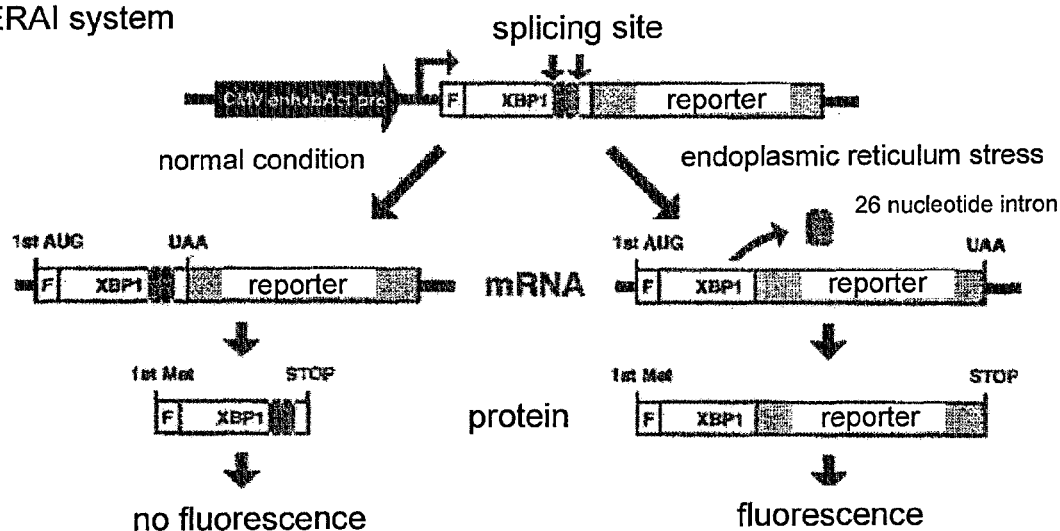
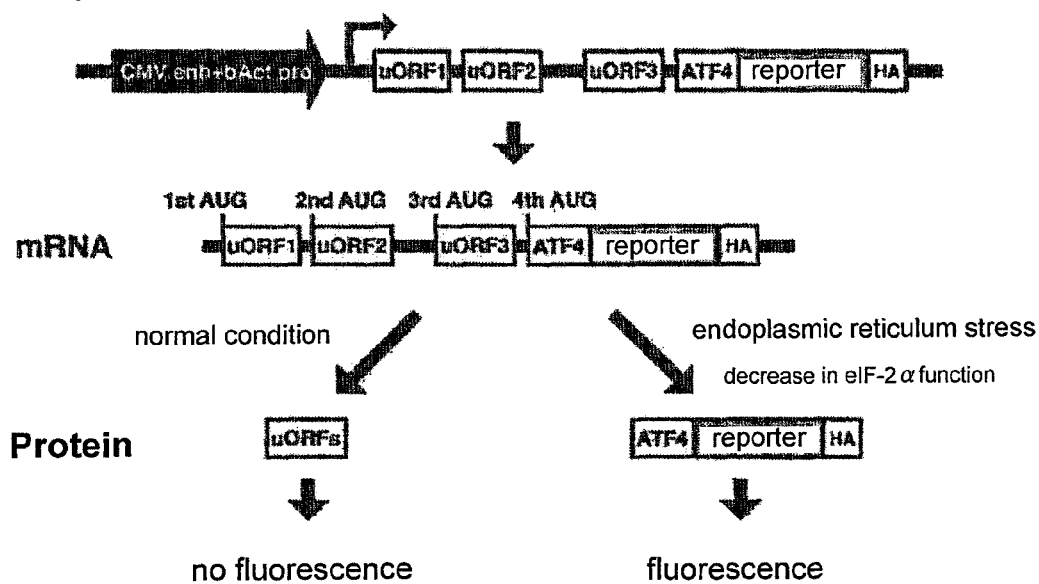


FIG. 18

## UMAI system



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# METHOD FOR SCREENING SUBSTANCE RELATING TO ENDOPLASMIC RETICULUM STRESS PARTICIPATING IN ONSET OF DIABETES

## TECHNICAL FIELD

The present invention relates to a method for screening an endoplasmic reticulum stressor or endoplasmic reticulum stress inhibitor; or a method for screening an antidiabetic drug candidate.

## BACKGROUND ART

A typical biological stress involved in the onset of diabetes is oxidative stress. Further, a new biological stress called endoplasmic reticulum stress has been found recently; research has gradually revealed that, similar to biological stress, endoplasmic reticulum stress is considered relevant to diabetes.

Endoplasmic reticulum stress designates an accumulation of irregular proteins in the endoplasmic reticulum. More specifically, endoplasmic reticulum stress is caused by failure of proper folding of proteins due to physical or chemical stimulation exerted on unstable incomplete proteins during the biosynthesis in the endoplasmic reticulum. In the endoplasmic reticulum, the unstable incomplete proteins during the biosynthesis are susceptible to physical or chemical stimulation, and such stimulation converts the proteins into abnormal proteins having an abnormal folding structure. Although the properly folded proteins are transported from the endoplasmic reticulum to the Golgi apparatus, the unfolded or misfolded proteins are stored inside the endoplasmic reticulum.

Cells are assumed to address endoplasmic reticulum stress using at least three methods below.

- (1) a method of increasing the amount of molecular chaperones or the like in the endoplasmic reticulum, thereby protecting the proteins accumulated in the endoplasmic reticulum (UPR: unfolded protein response);
- (2) a method of reducing the amount of protein entering into the endoplasmic reticulum, thereby reducing the load; and
- (3) a method of degrading proteins accumulated in the endoplasmic reticulum by cytoplasm (ERAD: ER-associated protein degradation).

However, when the stress significantly outperforms these defense mechanisms, or when the defense mechanisms malfunction due to some sort of error, the stress is assumed to result in cell death. The characteristics of such cell death resulting from endoplasmic reticulum stress is morphologically the same as apoptosis, and is accompanied by expression induction or activation of molecules called CHOP, JNK, and caspase.

Recent study has revealed that such cell death derived from endoplasmic reticulum stress is deeply involved in various diseases including neurodegenerative disorders such as diabetes, Parkinson's disease, Alzheimer's disease, polyglutamine disease, prion disease, or amyotrophic lateral sclerosis (ALS); and ischemic disorders. Therefore, finding a method of overcoming cell death originating from endoplasmic reticulum stress is believed to provide a new treatment for various diseases.

Under such circumstances, research on the measurement of endoplasmic reticulum stress or the discovery of substances involved in endoplasmic reticulum stress has been conducted in various fields (for example, see Patent Docu-

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ments 1 to 4). However, the relevance of certain substances to the mechanism of endoplasmic reticulum stress is still unclear.

## CITATION LIST

### Patent Documents

- [Patent Document 1] JP2008-131899A
- [Patent Document 2] JP2005-204516A
- [Patent Document 3] JP2005-065692A
- [Patent Document 4] JP2004-081143A

## SUMMARY OF INVENTION

### Technical Problem

As shown in FIG. 1, the endoplasmic reticulum stress that occurs in the endoplasmic reticulum is transmitted to cytoplasm through an endoplasmic reticulum membrane via three kinds of endoplasmic reticulum transmembrane proteins (IRE1 $\alpha$ , PERK, and ATF6). Further, the cellular response to the endoplasmic reticulum stress depends on whether all or a part of the pathways among the pathways corresponding to the three endoplasmic reticulum transmembrane proteins is activated, and depends on the type (IRE1 $\alpha$ , PERK, and/or ATF6) of the pathway activated. Therefore, in order to grasp the cellular response mechanism, or to establish a method for treating diabetes or neurodegenerative disorders caused by endoplasmic reticulum stress, it is very important to create a system for finding a certain substance or physiological/pathological environment that relates to activation of a certain pathway or all of the pathways mediated by the above three endoplasmic reticulum transmembrane proteins.

However, until now, among the pathways mediated by the above three endoplasmic reticulum transmembrane proteins, only a system for evaluating activations of pathways mediated by IRE1 $\alpha$  and PERK is known, and a system for evaluating activation of the pathway mediated by ATF6 has not been established. Further, when the system for evaluating pathway activation is used for screening an endoplasmic reticulum stressor, an endoplasmic reticulum stress inhibitor, or an antidiabetic drug candidate, the system must be capable of real-time evaluation of viable cells with a high degree of sensitivity, so as to enable rapid and highly accurate screening.

An object of the present invention is to provide a system for evaluating activation of the pathway mediated by ATF6. More specifically, an object of the present invention is to provide a method for screening an endoplasmic reticulum stressor that activates the pathway mediated by ATF6, and another object of the present invention is to provide a method for screening a substance that suppresses endoplasmic reticulum stress caused by activation of the pathway mediated by ATF6; and a method for screening an antidiabetic drug candidate.

### Technical Solution

As a result of extensive research, the inventors of the present invention found a method for real-time evaluation of activation of the pathway mediated by ATF6 in viable cells with a high degree of sensitivity. The method uses a nonfluorescent peptide domain derived from a fluorescent protein and a polynucleotide encoding the ATF6 protein domain.

Specifically, the present invention has the following aspects.



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Item 1. A polynucleotide encoding an amino acid sequence having a nonfluorescent peptide domain 1 derived from a fluorescent protein constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2, and an ATF6 protein domain.

Item 2. The polynucleotide according to Item 1, wherein the polynucleotide has a region encoding a nonfluorescent peptide domain 1 derived from a fluorescent protein at the 5' end, and a region encoding an ATF6 protein domain at the 3' end.

Item 3. The polynucleotide according to Item 1 or 2, wherein the polynucleotide encodes an amino acid sequence in which the nonfluorescent peptide domain 1 derived from a fluorescent protein and the ATF6 protein domain are connected via a spacer.

Item 4. A transgenic vector comprising the polynucleotide according to any one of Items 1 to 3.

Item 5. A transformant comprising a transgenic vector according to Item 4.

Item 6. The transformant according to Item 5, further comprising a nonfluorescent peptide domain 2 derived from a fluorescent protein constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2, and a polynucleotide encoding an amino acid sequence having a nuclear localization signal peptide domain, in a state where a protein having the amino acid sequence can be expressed.

Item 7. The transformant according to Item 6, wherein the transformant is a pancreatic  $\beta$ -cell comprising the vector of Item 4, a nonfluorescent peptide domain 2 derived from a fluorescent protein constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2, a polynucleotide encoding an amino acid sequence having a nuclear localization signal peptide domain, in a state where the protein having the amino acid sequence can be expressed.

Item 8-1. A method for screening an endoplasmic reticulum stressor, comprising the steps of:

(a) bringing an endoplasmic reticulum stressor candidate substance into contact with the transformant of Item 6;

(b) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor candidate substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant not in contact with the endoplasmic reticulum stressor candidate substance; and

(c) selecting the endoplasmic reticulum stressor candidate substance as an endoplasmic reticulum stressor when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor candidate substance is higher than the fluorescence intensity of the control transformant.

Item 8-2. A method for screening an organ-specific endoplasmic reticulum stressor, comprising the steps of:

(a') bringing an organ-specific endoplasmic reticulum stressor candidate substance into contact with the transformant of Item 6;

(b') measuring the fluorescence intensity of the transformant in contact with the organ-specific endoplasmic reticulum stressor candidate substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant not in contact with the organ-specific endoplasmic reticulum stressor candidate substance; and

(c') selecting the organ-specific endoplasmic reticulum stressor candidate substance as an organ-specific endoplasmic reticulum stressor when the fluorescence intensity of the transformant in contact with the organ-specific endoplasmic reticulum stressor candidate substance is higher than the fluorescence intensity of the control transformant.

Item 9-1. The method according to Item 8-1 or 8-2, wherein the endoplasmic reticulum stressor is an endoplasmic reticu-

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lum stressor that activates ATF6 pathway, but does not activate IRE1 $\alpha$  pathway or PERK pathway; or an endoplasmic reticulum stressor that activates ATF6 pathway, and IRE1 $\alpha$  pathway and/or PERK pathway.

Item 9-2. The method according to Item 8-1 or 8-2, wherein the endoplasmic reticulum stressor is:

an endoplasmic reticulum stressor that activates ATF6 pathway, but does not activate IRE1 $\alpha$  pathway or PERK pathway,

an endoplasmic reticulum stressor that activates ATF6 pathway, and IRE1 $\alpha$  pathway and/or PERK pathway, or

an endoplasmic reticulum stressor that does not activate ATF6 pathway, but activates IRE1 $\alpha$  pathway and/or PERK pathway.

Item 10-1. A method for screening an endoplasmic reticulum stress inhibitor, comprising the steps of:

(d) bringing an endoplasmic reticulum stressor and a test substance with the transformant of Item 6;

(e) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant that is not in contact with the test substance, but that is in contact with the endoplasmic reticulum stressor; and

(f) selecting the test substance as an endoplasmic reticulum stress inhibitor when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance is higher than the fluorescence intensity of the control transformant.

Item 10-2. A method for screening a substance for organ-specifically suppressing endoplasmic reticulum stress, comprising the steps of:

(d') bringing an endoplasmic reticulum stressor and a test substance with the transformant of Item 6;

(e') measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant that is not in contact with the test substance but that is in contact with the endoplasmic reticulum stressor; and

(f') selecting the test substance as a substance for organ-specifically suppressing endoplasmic reticulum stress when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance is higher than the fluorescence intensity of the control transformant.

Item 11. A method for screening an antidiabetic drug candidate, comprising the steps of:

(g) bringing an endoplasmic reticulum stressor and a test substance with the transformant of Item 7;

(h) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant that is not in contact with the test substance but in contact with the endoplasmic reticulum stressor; and

(i) selecting the test substance as an antidiabetic drug candidate when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance is higher than the fluorescence intensity of the control transformant.

#### Advantageous Effects of Invention

The present invention is characterized by using a polynucleotide encoding a nonfluorescent peptide domain 1 derived from a fluorescent protein constituted of a nonfluor-

rescent peptide domain 1 and a nonfluorescent peptide domain 2; and the ATF6 protein domain. The present invention having such a characteristic enables real-time evaluation of activation of the pathway mediated by ATF6 in viable cells with a high degree of sensitivity. More specifically, the screening method of the present invention enables determination as to whether a given substance or a given physiological/pathological environment serves as an endoplasmic reticulum stressor that activates the pathway mediated by ATF6. The screening method of the present invention further enables determination (screening) as to whether a test substance is an endoplasmic reticulum stress inhibitor that suppresses endoplasmic reticulum stress caused by activation of the pathway mediated by ATF6. Furthermore, the screening method of the present invention enables screening of an antidiabetic drug candidate.

Further, the screening method of the present invention makes it possible to, for the first time, perform evaluation of endoplasmic reticulum stress mediated by the three pathways (the three pathways individually mediated by IRE1 $\alpha$ , PERK, and ATF6) involved in endoplasmic reticulum stress response simultaneously and in the same cells. Using this evaluation of the present invention, it was discovered that the degree of response to endoplasmic reticulum stress varies between the three pathways for each cell group derived from a different organ.

#### BRIEF DESCRIPTION OF DRAWINGS

FIG. 1 shows three pathways activated by endoplasmic reticulum stress, and an example of an endoplasmic reticulum stress response caused by the activation of the three pathways.

FIG. 2 shows a function of ATF6 protein in a cell. Panel (A) shows a function of ATF6 protein in a cell with no stress. Panel (B) shows a function of ATF6 protein in a cell with stress.

FIG. 3 shows a principle of the screening method of the present invention.

FIG. 4 shows a DNA sequence (SEQ ID NO: 17) inserted in an EGFP-ATF6d expression vector.

- 1) green fluorescent protein cDNA fragment
- 2) spacer
- 3) 3XFLAG tag
- 4) nuclear localization signal
- 5) PEST sequence
- 6) partial cDNA fragment of mice ATF6 $\alpha$

FIG. 5 shows a DNA sequence (SEQ ID NO: 24) inserted in an EGFP expression vector.

- 7) nuclear localization signal
- 8) green fluorescent protein cDNA fragment.

FIG. 6 shows a result of confirmation of the function of an ATF6 activity reporter system.

FIG. 7 shows a result of confirmation of the endoplasmic reticulum stress specificity of an ATF6 activity reporter system.

FIG. 8 shows a result of confirmation of the specificity of an endoplasmic reticulum stress response pathway of the ATF6 activity reporter system.

FIG. 9 shows a DNA sequence (SEQ ID NO: 27 and 28) used for production of an EGFP-ATF6d expression vector in which the spacer is changed to GGGs (SEQ ID NO: 5) or GGGSGGGSGGGs (SEQ ID NO: 6).

FIG. 10 shows a result of confirmation of the importance of the spacer in the EGFP-ATF6d expression vector. The results of spacer GGGs (SEQ ID NO: 5), spacer GGGSGGGs (SEQ ID NO: 10), and spacer GGGSGGGSGGGs (SEQ ID NO: 6) are shown.

FIG. 11 shows a result of confirmation of the importance of PEST sequence in an EGFP-ATF6d expression vector.

FIG. 12 shows a vector map of an Ire1 activation reporter vector for measuring Ire1 pathway by XBP splicing, and a vector map of a PERK activation reporter expression vector for measuring PERK pathway by ATF4 translation.

FIG. 13 shows the difference between endoplasmic reticulum stress response signals of different organs (fluorescence microscope image).

FIG. 14 shows the difference between endoplasmic reticulum stress response signals of different organs (measurement results of fluorescence intensity).

FIG. 15 shows inhibition of insulin secretion in pancreatic  $\beta$ -cells by an insulin endoplasmic reticulum stressor.

FIG. 16 shows a sensitivity during the detection of ATF6 pathway activation using a ATF6 activity reporter system, which is superior to the sensitivity during the detection using a hitherto-known method (western blotting).

FIG. 17 shows a gene architecture in ERAI system, and a mechanism of ERAI system.

FIG. 18 shows a gene architecture in UMAI system, and a mechanism of UMAI system.

#### DESCRIPTION OF EMBODIMENTS

##### (1) the Principle of the Present Invention

The principle of the present invention is described below in reference to FIGS. 2 and 3.

The fluorescent protein of the present invention is constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2. The nonfluorescent peptide domain 1 and the nonfluorescent peptide domain 2 are derived from the same fluorescent protein, and correspond to two fragments obtained by dividing a fluorescent protein in the molecule. Accordingly, when the nonfluorescent peptide domain 1 is an N-terminus fragment, the nonfluorescent peptide domain 2 is a C-terminus fragment. Conversely, when the nonfluorescent peptide domain 1 is a C-terminus fragment, the nonfluorescent peptide domain 2 is an N-terminus fragment. The nonfluorescent peptide domains 1 and 2 do not independently have fluorescence activity; however, they exhibit fluorescence activity as they are associated in a cell.

ATF6 protein is constituted of an endoplasmic reticulum lumen domain ("A" in FIG. 2), a transmembrane domain ("B" in FIG. 2), and a cytoplasmic domain ("C" in FIG. 2). ATF6 protein is present in a cell while penetrating the endoplasmic reticulum membrane ("ER" in FIG. 2). In response to endoplasmic reticulum stress that activates a pathway mediated by ATF6 protein, the part corresponding to the cytoplasmic domain of ATF6 protein ("C" in FIG. 2) is separated. The separated cytoplasmic domain ("C" in FIG. 2) is transferred to a nucleus ("Nuc" in FIG. 2) by a nuclear localization signal inherent in the domain, and serves as a transcription factor that adjusts the transcription of the gene group involved in the endoplasmic reticulum stress response. The present invention uses this mechanism to create a system for evaluating endoplasmic reticulum stress that activates the pathway mediated by ATF6. The evaluation system of the present invention operates as follows (see FIG. 3).

The fusion protein of the nonfluorescent peptide domain 1 derived from a fluorescent protein ("GFP-S" in FIG. 3; hereinafter referred to as "nonfluorescent peptide domain 1") expressed in a cell, and a ATF6 protein domain ("A," "B," and "C" in FIG. 3) is disposed on the endoplasmic reticulum membrane by the transmembrane domain ("B" in FIG. 3) of ATF6 protein domain. By this placement of the fusion protein, the endoplasmic reticulum lumen domain ("A" in FIG.

3) in the ATF6 protein domain is present in the endoplasmic reticulum lumen, and the nonfluorescent peptide domain 1 ("GFP-S" in FIG. 3), and the cytoplasmic domain ("C" in FIG. 3) in the ATF6 protein domain are present in the cytoplasm.

Further, under the endoplasmic reticulum stress, the nonfluorescent peptide domain 1 ("GFP-S" in FIG. 3), and the cytoplasmic domain ("C" in FIG. 3) in the ATF6 protein domain are cleaved from the endoplasmic reticulum membrane, and transferred into the nucleus by a nuclear localization signal in the ATF6 protein domain or a nuclear localization signal artificially introduced into the fusion protein.

The nonfluorescent peptide domain 1 ("GFP-S" in FIG. 3) in the fusion protein transferred into the nucleus is associated with the fluorescent protein-derived nonfluorescent peptide domain ("GFP-L" in FIG. 3) present in the same nucleus. By the association, the original fluorescence activity of the fluorescent protein recovers. The recovery of the fluorescence activity can be confirmed by the presence of fluorescence generated in response to irradiation of excitation light of a wavelength corresponding to the type of the fluorescent protein.

More specifically, the endoplasmic reticulum stress mediated by ATF6 can be evaluated by detecting a fluorescence.

#### (2) Polynucleotide of the Present Invention

The polynucleotide of the present invention is a polynucleotide encoding an amino acid sequence having a nonfluorescent peptide domain 1 derived from a fluorescent protein constituted of nonfluorescent peptide domain 1 and nonfluorescent peptide domain 2; and an ATF6 protein domain.

#### (2-1) Nonfluorescent Peptide Domain 1 of the Present Invention Derived from a Fluorescent Protein (Hereinafter Referred to as Nonfluorescent Peptide Domain 1 of the Present Invention)

The fluorescent protein is not particularly limited insofar as it loses the fluorescence activity by the division in the molecule, and gains the fluorescence activity again as the divided fragments are associated. Preferable examples of fluorescent proteins include GFP, GFP mutants, and a GFP-like protein family not derived from GFP. Among them, GFP and GFP mutants are particularly preferable. GFP is a green fluorescent protein derived from *Aequorea victoria*. The amino acid sequence of GFP is represented by amino acid SEQ ID NO: 4.

Further, the fluorescent protein may be modified by substitution, deletion, or addition of one or more amino acids insofar as it loses the fluorescence activity by the division in the molecule, and gains the fluorescence activity again as the divided fragments are associated.

As for the substitution, so as to maintain the protein structure, the amino acid may be substituted with an amino acid similar to the original amino acid (the amino acid before substitution) in terms of polarity, electric charge, solubility, hydrophilicity/hydrophobicity, polarity, and the like. According to the amino acid classification, glycine, alanine, valine, leucine, isoleucine, and proline are classified into nonpolar amino acids; serine, threonine, cysteine, methionine, asparagine, and glutamine are classified into polar amino acids; phenylalanine, tyrosine, and tryptophan are classified into amino acids having aromatic side chain; lysine, arginine, and histidine are classified into basic amino acids; and aspartic acid and glutamic acid are classified into acidic amino acids. The substitution is performed using a protein in the same protein group.

The GFP mutants are obtained by substituting at least one amino acid in GFP. By the substitution, a GFP mutant is modified in fluorescence intensity, excite wavelength, fluorescence wavelength, and stability in a cell. Examples of GFP

mutants include EGFP, YFP, CFP, and RFP. The amino acid sequence of EGFP is represented by amino acid SEQ ID NO: 1.

The fluorescent protein, which belongs to the GFP-like protein family, has a structure similar to GFP (having a helix tissue of eleven  $\beta$ -sheets, which further forms a cylindrical structure by covering the chromophore (white portion). Examples of fluorescent proteins include CopGFP derived from crustaceans, and DsRed derived from sea anemone.

Various examples of GFP mutants and fluorescent proteins belonging to the GFP-like protein family are disclosed in published documents, including Document 1 (Appl. Microbiol. Biotechnol. (2007) 77:1-12).

The nonfluorescent peptide domain 1 of the present invention is an N-terminus fragment or a C-terminus fragment obtained by dividing a fluorescent protein in the molecule. The division site is not limited insofar as the division deactivates the fluorescence activity of each fragment (the N-terminus fragment and the C-terminus fragment) and the fluorescence activity is recovered by the reunion of the two divided fragments. The division site can be determined by referring to published documents, including Document 2 (Nature Biotechnology, 2003, vol. 21, 539-545). For example, for EGFP, the division site is preferably one of the 195th to 226th amino acids in SEQ ID NO: 1, more preferably one of the 205th to 222nd amino acids in SEQ ID NO: 1, particularly preferably one of the 212th to 218th amino acids in SEQ ID NO: 1. Further, in these examples, it is preferable to use a C-terminus fragment as the nonfluorescent peptide domain 1 of the present invention.

#### (2-2) ATF6 Protein Domain of the Present Invention

The biological species to be used to obtain ATF6 protein include not only mice (*Mus musculus*), but also other biological species having a genomic region encoding ATF6 protein having an amino acid sequence identity of preferably not less than 70%, more preferably not less than 80%, further preferably not less than 85%, further more preferably not less than 90%, particularly preferably not less than 95% with the mice ATF6 protein. Examples of such biological species include rodents such as rats; and mammals such as rabbit, apes, and humans (*Homo sapiens*). Humans (*Homo sapiens*) and mice (*Mus musculus*) are most preferable biological species.

ATF6 protein is constituted of a cytoplasmic domain, an endoplasmic reticulum transmembrane domain, and an endoplasmic reticulum lumen domain. When the biological species is a mouse, ATF6 protein has an amino acid sequence of SEQ ID NO: 2, or an amino acid sequence having an identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the amino acid sequence of SEQ ID NO: 2. When the biological species is a human, the ATF6 protein has an amino acid sequence of SEQ ID NO: 3, or an amino acid sequence having an identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the amino acid sequence of SEQ ID NO: 3. When the biological species is a mouse, a region of the 1st to 364th amino acids in the amino acid sequence of SEQ ID NO: 2 corresponds to the cytoplasmic domain, a region of the 365th to 384th amino acids in the amino acid sequence of SEQ ID NO: 2 corresponds to the endoplasmic reticulum transmembrane domain, and a region of the 385th to 656th amino acids in the amino acid sequence of SEQ ID NO: 2 corresponds to the endoplasmic reticulum lumen domain. When the biological species is a human, a region of the 1st to 377th amino acids in the amino acid sequence of SEQ ID NO: 3 corresponds to the cytoplasmic domain, a region of the 378th to 398th amino acids in the amino acid sequence of SEQ ID NO: 3 corresponds to the endoplasmic reticulum

transmembrane domain, and a region of the 399th to 670th amino acids in the amino acid sequence of SEQ ID NO: 3 corresponds to the endoplasmic reticulum lumen domain.

The ATF6 protein domain of the present invention includes a nuclear localization signal peptide region (a nuclear localization signal peptide in ATF6 protein and/or an exogenous nuclear localization signal peptide), a region involved in the division by endoplasmic reticulum stress, an endoplasmic reticulum transmembrane domain, and a portion receiving endoplasmic reticulum stress in the endoplasmic reticulum lumen domain. Insofar as it is within the above-listed domains, the ATF6 protein domain may be the entire length of the ATF6 protein.

The nuclear localization signal in the ATF6 protein is represented by the amino acid sequence RKKKKE (SEQ ID NO: 7). When the biological species is a mouse, the nuclear localization signal corresponds to a region of the 311th to 316th amino acids in the amino acid sequence of SEQ ID NO: 2. When the biological species is a human, the nuclear localization signal corresponds to a region of the 324th to 329th amino acids in the amino acid sequence of SEQ ID NO: 3.

A hitherto-known signal peptide, such as DPKKKRKV (SEQ ID NO: 8), may be used as the exogenous nuclear localization signal peptide. The nuclear localization signal peptide may also be a repetition of the sequence of a hitherto-known signal peptide.

The portion receiving endoplasmic reticulum stress in the endoplasmic reticulum lumen domain is a region that receives endoplasmic reticulum stress and causes the division of the ATF6 cytoplasmic domain.

The region involved in the division by endoplasmic reticulum stress is a region of the 365th to 411th amino acids in the amino acid sequence of SEQ ID NO: 2 when the biological species is a mouse, and is a region of the 378th to 424th amino acids in the amino acid sequence of SEQ ID NO: 3 when the biological species is a human.

The ATF6 protein domain of the present invention is not limited insofar as the domain has the nuclear localization signal peptide region (a nuclear localization signal peptide in ATF6 protein and/or an exogenous nuclear localization signal peptide), the region involved in the division by endoplasmic reticulum stress, the endoplasmic reticulum transmembrane domain, and the portion receiving endoplasmic reticulum stress in the endoplasmic reticulum lumen domain. However, when the biological species is a mouse, the ATF6 protein domain of the present invention is a domain having a region of the 100th to 656th amino acids in the ATF6 protein amino acid sequence of SEQ ID NO: 2, or an amino acid region having an amino acid identity of not less than 90%, preferably not less than 95%, more appropriately not less than 98% with the above amino acid region; more preferably, the ATF6 protein domain is a domain having a region of the 250th to 656th amino acids in the ATF6 protein amino acid sequence of SEQ ID NO: 2, or an amino acid region having an amino acid identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the above amino acid region; particularly preferably, the ATF6 protein domain is a domain having an exogenous nuclear localization signal peptide region and a region of the 360th to 656th amino acids in the ATF6 protein amino acid sequence of SEQ ID NO: 2, or an amino acid region having an amino acid identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the above amino acid region. When the biological species is a human, the ATF6 protein domain of the present invention is preferably a domain having a region of the 100th to 670th amino acids in the ATF6 protein amino acid sequence of SEQ ID NO: 3, or an amino acid region having an

amino acid identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the above amino acid region; more preferably, the ATF6 protein domain is a domain having a region of the 250th to 670th amino acids in the amino acid sequence of SEQ ID NO 3, or an amino acid region having an amino acid identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the above amino acid region; particularly preferably, the ATF6 protein domain is a domain having an exogenous nuclear localization signal peptide region and a region of the 373rd to 670th amino acids in the ATF6 protein amino acid sequence of SEQ ID NO: 3, or an amino acid region having an amino acid identity of not less than 90%, preferably not less than 95%, more preferably not less than 98% with the above amino acid region.

The ATF6 protein domain may be a domain resulting from substitution, deletion, or addition of one or more amino acids in the above-listed domain examples. Such a mutation may be suitably conducted insofar as the functions of the nuclear localization signal peptide region, the portion receiving endoplasmic reticulum stress in the endoplasmic reticulum lumen domain, the endoplasmic reticulum transmembrane domain, and the portion divided by endoplasmic reticulum stress in the cytoplasmic domain are obtained.

As for the substitution, so as to maintain the protein structure, the amino acid may be substituted with an amino acid similar to the original amino acid (the amino acid before substitution) in terms of polarity, electric charge, solubility, hydrophilicity/hydrophobicity, polarity, and the like. According to the amino acid classification, glycine, alanine, valine, leucine, isoleucine, and proline are classified into nonpolar amino acids; serine, threonine, cysteine, methionine, asparagine, and glutamine are classified into polar amino acids; phenylalanine, tyrosine, and tryptophan are classified into amino acids having an aromatic side chain; lysine, arginine, and histidine are classified into basic amino acids; and aspartic acid and glutamic acid are classified into acidic amino acids. The substitution is performed using a protein in the same protein group.

(2-3) Dispositions of Nonfluorescent Peptide Domain 1 and ATF6 Protein Domain

In the present invention, the locations of the two domains in the polynucleotide encoding the nonfluorescent peptide domain 1 and the ATF6 protein domain are not particularly limited. However, it is preferable that the region encoding the nonfluorescent peptide domain 1 is located at the 5' end, and that the region encoding the ATF6 protein domain is located at the 3' end.

Further, the nonfluorescent peptide domain 1 derived from a fluorescent protein and the ATF6 protein domain are preferably disposed having a spacer therebetween.

The spacer used in the present invention designates an amino acid sequence derived from a natural protein or a synthetic amino acid sequence. Although the amino acid sequence of the spacer is not particularly limited, the sequence is preferably an amino acid sequence that does not form a secondary structure, such as the  $\alpha$ -helix structure or the  $\beta$ -sheet structure; and that can be freely folded. Examples of the amino acid sequence of the spacer include the four residues GGGS, and a repetition of this sequence.

The number of the amino acid residues of the spacer is preferably not less than 3, more preferably 4 to 50, further preferably 6 to 20, particularly preferably 7 to 15. In the present invention, if the number of amino acid residues of the spacer is too small, the association of the nonfluorescent peptide domains 1 and 2 derived from a fluorescent protein is assumed to be hindered by the ATF6 protein domain; and the

desired fluorescence detection sensitivity in the method for screening an endoplasmic reticulum stressor, an endoplasmic reticulum stress inhibitor, or an antidiabetic drug candidate using the polynucleotide of the present invention is not ensured.

#### (2-4) Other Sequences

The polynucleotide of the present invention may contain other sequences including a polynucleotide encoding a protein tag, and polynucleotides encoding other peptides.

FLAG tag, His tag, GST tag, and the like, may be used as the protein tag. The protein tag may also be a repetition of the above tag sequence.

Other examples of peptide include PEST sequences. Insertion of a PEST sequence promotes degradation of the fusion protein. The PEST sequence is not particularly limited, and hitherto-known PEST sequences may be used insofar as the desired function is ensured. Examples thereof include the amino acid sequence of SHGFPPEVEEQDDGTLPM-SCAQESGMDRHPAACASARINV (SEQ ID NO: 9). The location of the PEST sequence is not particularly limited insofar as the desired function is ensured; however, the PEST sequence is preferably disposed between the nonfluorescent peptide domain 1 and the ATF6 protein domain. Although the PEST sequence is not indispensable in the present invention, the insertion of a PEST sequence reduces the background fluorescence during the method for screening an endoplasmic reticulum stressor, an endoplasmic reticulum stress inhibitor, or an antidiabetic drug candidate using the polynucleotide of the present invention, thereby enabling fluorescence detection with a high degree of sensitivity.

#### (3) Production Method of Polynucleotide of the Present Invention

The polynucleotide of the present invention can be synthesized through artificial gene synthesis, or nucleic acid amplification (PCR, etc.) using a commercially available polynucleotide or a polynucleotide from a cDNA library. The polynucleotides encoding the above domains may be connected through a hitherto-known gene linkage technology by adding a hitherto-known restriction enzyme sequence at both ends.

Various expression vectors having a polynucleotide encoding a fluorescent protein are commercially available (for example, products of Clontech). The sequence data of the polynucleotide is also published.

The polynucleotide encoding the ATF6 protein domain can be obtained, for example, by creating a primer of an appropriate site based on the ATF6 gene sequence published in the NCBI database or other gene databases, and producing a polynucleotide through a gene amplification technology using a corresponding primer obtained from a cDNA library.

The other sequences inserted in the polynucleotide of the present invention, such as the polynucleotide sequence encoding a protein tag, the polynucleotide sequence encoding a nuclear localization signal, or the polynucleotide sequence encoding a PEST sequence, are open to the public. Therefore, these sequences can be obtained, for example, using artificial gene synthesis technology by referring to published sequence data.

#### (4) Transgenic Vector of the Present Invention

The transgenic vector of the present invention is a transgenic vector containing the polynucleotide of the present invention, and can be obtained by connecting the polynucleotide of the present invention to an appropriate vector.

The vector is not particularly limited insofar as it contains the polynucleotide of the present invention; however, the vector is preferably capable of enabling expression of the fusion protein resulting from the polynucleotide of the

present invention in eukaryote cells, more preferably in animal cells, further preferably in mammal animal cells, particularly preferably in rodent (in particular, mice) or human cells. Specific examples of vectors include *Escherichia coli* vectors pBR322, pUC19, pKK233-2, pET21a, and the like; yeast vectors Yip5, Yrp17, Yep24, and the like; and animal cell vectors pcDNA, pBAC, and the like.

The above transgenic vector preferably contains a marker gene to enable selection of the transformed cells. Examples of marker genes include genes for complementing auxotrophy of the host, or drug-resistant genes. Further, the transgenic vector preferably also contains a promoter or other control sequences (for example, an enhancer sequence, a terminator sequence, a polyadenylation sequence, and the like) for enabling expression of the above genes in the host. Examples of promoters include SV40, CMV, ie1, T7, lac, trp, and tac.

#### (5) Transformant of the Present Invention

A transformant containing the above transgenic vector can be obtained by transforming a host using the transgenic vector.

The host is not particularly limited insofar as it is transformable by the transgenic vector of the present invention. Examples of hosts include cells such as *Escherichia coli*, yeasts, filamentous fungi, and animal cells. Among them, it is preferable to use eukaryote cells, more preferably animal cells, and further preferably rodent (in particular, mice) or human cells. Further, when the host is animal cells, the host cells may be obtained from various organs including pancreatic cells, kidney cells, hepatic cells, adipose cells, and skeletal cells. When the transformant is used for the method for screening an antidiabetic drug candidate, the host cells are preferably pancreatic cells. Among pancreatic cells, pancreatic  $\beta$ -cells are more preferable.

The transformation may be performed using a hitherto-known method according to the type of the host. Examples of the hitherto-known methods include a calcium chloride method, electroporation method, lipofection method, and DEAF dextran method. The transformant of the present invention may be selected from the thus-obtained transformants based on a drug resistance marker, etc., of the vector.

Further, the transformant of the present invention preferably contains a polynucleotide encoding an amino acid sequence having a nonfluorescent peptide domain 2 derived from a fluorescent protein constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2 (hereinafter, the domain referred to as "nonfluorescent peptide domain 2" designates this protein), and a nuclear localization signal peptide domain while ensuring a condition where the protein having the amino acid sequence can be expressed. This transformant (hereinafter referred to as "screening transformant") may be used for the later-described screening method. Further, a screening transformant obtained by using pancreatic  $\beta$ -cells as the host (hereinafter referred to as "antidiabetic drug candidate screening transformant") may be suitable for the later-described screening method, in particular, the method for screening antidiabetic drug candidates.

The nonfluorescent peptide domain 2 is an N-terminus fragment or a C-terminus fragment generated by dividing a fluorescent protein in the molecule. The nonfluorescent peptide domain 2 is obtained from the same fluorescent protein from which the aforementioned nonfluorescent peptide domain 1 is obtained. The nonfluorescent peptide domains 1 and 2 correspond to the two fragments resulting from the division of a fluorescent protein. Therefore, when the nonfluorescent peptide domain 1 is an N-terminus fragment, the nonfluorescent peptide domain 2 is a C-terminus fragment.

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The N-terminus fragment and the C-terminus fragment can be arbitrarily used as the nonfluorescent peptide domain 1 or 2. However, it is preferable that the nonfluorescent peptide domain 1 be a C-terminus fragment, and that the nonfluorescent peptide domain 2 be an N-terminus fragment.

A hitherto-known signal peptide, such as Asp-Pro-Lys-Lys-Lys-Arg-Lys-Val (SEQ ID NO: 8), may be used as the nuclear localization signal peptide domain. The nuclear localization signal peptide domain may also be a repetition of a sequence of a hitherto-known signal peptide.

The state where "the protein can be expressed" is not particularly limited insofar as the protein constituted of an amino acid sequence containing the nonfluorescent peptide domain 2, and the nuclear localization signal peptide domain can be expressed in the cells. However, the 5' end of the polynucleotide encoding an amino acid sequence having a nonfluorescent peptide domain 2 and a nuclear localization signal peptide domain preferably has a promoter sequence.

A hitherto-known sequence may be used as the promoter sequence. Examples of the promoter sequence include CMV promoter sequence, SV40 promoter, and the like.

#### (6) the Screening Method of the Present Invention

Using the above transformant, it is possible to screen an endoplasmic reticulum stressor, an endoplasmic reticulum stress inhibitor, or an antidiabetic drug candidate.

#### (6-1) A Method for Screening Endoplasmic Reticulum Stressor

The method for screening an endoplasmic reticulum stressor includes a step of (a) bringing an endoplasmic reticulum stressor candidate substance into contact with the screening transformant described in "(5) Transformant of the Present Invention"; a step of (b) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor candidate substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant not in contact with the endoplasmic reticulum stressor candidate substance; and a step of (c) selecting the endoplasmic reticulum stressor candidate substance as an endoplasmic reticulum stressor when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor candidate substance is higher than the fluorescence intensity of the control transformant.

The type of the substance as a candidate for endoplasmic reticulum stressor is not particularly limited. Examples of candidates include proteins, peptides, non-peptidic compounds (nucleotides, amines, saccharides, lipids, etc.), organic low-molecular-weight compounds, inorganic low-molecular-weight compounds, fermentation products, cell extracts, plant extracts, and animal tissue extracts.

The step of bringing the endoplasmic reticulum stressor candidate substance into contact with the cells may be performed under conditions (in terms of temperature, pH, components of culture medium) in which the cells are kept alive and the fusion protein of the nonfluorescent peptide domain 1 derived from a fluorescent protein and the ATF6 protein domain, and the protein containing a nonfluorescent peptide domain 2 derived from a fluorescent protein can be expressed from the introduced transgenic vector. The concentration of the endoplasmic reticulum stressor candidate substance to be brought into contact with the cells varies depending on the type of the substance. For example, the concentration is about 0.001 to 100  $\mu\text{g/ml}$ .

The fluorescence detection may be performed by generating fluorescence by emission of excitation light having a wavelength suitable for a fluorescent protein.

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The method for measuring the fluorescence intensity is not particularly limited insofar as it enables comparison of the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor with the fluorescence intensity of the control transformant not in contact with the endoplasmic reticulum stressor. For example, the fluorescence intensity measurement may be performed by capturing an image of the fluorescing transformant into a computer, and determining a color depth corresponding to the fluorescence in the image.

Further, screening of an organ-specific endoplasmic reticulum stressor becomes possible by using the transformant of the present invention derived from the target organ. For example, screening of a liver-specific endoplasmic reticulum stressor may be performed using a transformant of the present invention that is obtained using hepatic cells as the host.

Furthermore, by combining the screening method of the present invention with a hitherto-known screening method, it is possible to determine whether the endoplasmic reticulum stressor is:

an endoplasmic reticulum stressor that activates ATF6 pathway, but does not activate IRE1 $\alpha$  pathway or PERK pathway; an endoplasmic reticulum stressor that activates ATF6 pathway, IRE1 $\alpha$  pathway, and/or PERK pathway; or an endoplasmic reticulum stressor that does not activate ATF6 pathway, but activates IRE1 $\alpha$  pathway and/or PERK pathway.

More specifically, it is possible to determine whether the endoplasmic reticulum stressor is:

(o) an endoplasmic reticulum stressor that activates ATF6 pathway, but does not activate IRE1 $\alpha$  pathway or PERK pathway;

(p) an endoplasmic reticulum stressor that activates ATF6 pathway and IRE1 $\alpha$  pathway, but does not activate PERK pathway;

(q) an endoplasmic reticulum stressor that activates ATF6 pathway and PERK pathway, but does not activate IRE1 $\alpha$  pathway;

(r) an endoplasmic reticulum stressor that activates ATF6 pathway, IRE1 $\alpha$  pathway, and PERK pathway;

(s) an endoplasmic reticulum stressor that does not activate ATF6 pathway, but activates IRE1 $\alpha$  pathway and PERK pathway;

(t) an endoplasmic reticulum stressor that does not activate ATF6 pathway and IRE1 $\alpha$  pathway, but activates PERK pathway; or

(u) an endoplasmic reticulum stressor that does not activate ATF6 pathway and PERK pathway, but activates IRE1 $\alpha$  pathway.

The hitherto-known screening method is a method capable of selecting whether the endoplasmic reticulum stressor candidate substance activates IRE1 $\alpha$  pathway and/or PERK pathway. For example, the method disclosed in JP2005-204516A may be used. Therefore, by combining such a hitherto-known screening method with the method of the present invention capable of screening an endoplasmic reticulum stressor that activates ATF6 pathway from multiple endoplasmic reticulum stressor candidate substances, it becomes possible to determine which of the endoplasmic reticulum stressors (o) to (u) corresponds to the endoplasmic reticulum stressor activating ATF6 pathway. Further, the combination of the method of the present invention with the hitherto-known screening method also enables screening of an endoplasmic reticulum stressor that does not activate ATF6 pathway.

The method disclosed in JP2005-204516A is specifically described below.

The cells used in this method are transgenic cells containing:

(v) an expression vector containing a fusion gene of XBP1 gene and a gene encoding a first reporter protein; the expression vector being disposed so that the fusion protein of XBP1 protein and the first reporter protein is expressed only when XBP1 gene is spliced; and

(w) an expression vector containing a fusion gene of ATF4 gene and a gene encoding a second reporter protein; the gene encoding the second reporter protein being disposed downstream of the true translation start point of ATF4 gene.

Using the above transgenic cells, it is possible to select whether a candidate substance is an endoplasmic reticulum stressor that activates IRE1 $\alpha$  pathway and/or PERK pathway through the following method including:

(x) a step of bringing the transgenic cells into contact with a candidate substance,

(y) a step of measuring the activities of the first reporter protein and the second reporter protein in the transgenic cells; and

(z) a step of, in the transgenic cell, determining the candidate substance as an endoplasmic reticulum stressor that activates IRE1 $\alpha$  pathway but does not activate PERK pathway when the activity of the first reporter protein is detected and the activity of the second reporter protein is not detected; and when the activity of the first reporter protein is not detected and the activity of the second reporter protein is detected, determining the candidate substance as an endoplasmic reticulum stressor that activates PERK pathway and does not activate IRE1 $\alpha$  pathway; and when the activities of the first reporter protein and the second reporter protein are both detected, determining the candidate substance as an endoplasmic reticulum stressor that activates IRE1 $\alpha$  pathway and PERK pathway.

#### Gene for ERAI System

As shown in FIG. 17, the expression vector (v) is structured to activate the ERAI system. The expression vector (v) contains a fusion gene of XBP1 gene and a gene encoding the first reporter protein, and is disposed so that the fusion protein of XBP1 protein and the first reporter protein is expressed only when XBP1 gene is spliced.

XBP1 gene is one of the stimulus response genes. Under endoplasmic reticulum stress, IRE1 splices a 26 nucleotide intron of XBP1. Examples of known cDNA sequences of XBP1 include XBP1 of human, bovine, mice, *Xenopus laevis*, and zebra fish. They are registered in the EST database as BE170119, AV604667, BF143019, AF358133, and AF399918, respectively. In the present invention, cDNA of human XBP1 (hereinafter referred to as "Sequence 1"), NCBI registration No. AB076383, is used as an example of cDNA of XBP1. During the absence of splicing, the positions 9 to 794 of Sequence 1 serve as a code-coding region, and are translated into an XBP1 protein (truncated protein) having 261 amino acid residues (hereinafter referred to as "Sequence 2"). On the other hand, the intron of cDNA corresponds to a base sequence at positions 50 to 527 of Sequence 1. The splicing of XBP1 gene by IRE1 results in a frameshift that allows positions 9 to 501 and 528 to 1165 of Sequence 1 to serve as a coding region, thus translating XBP1 into an active XBP1 protein having 376 amino acid residues.

The gene encoding the first reporter protein is fused to an appropriate position in the downstream of the active XBP1 protein coding region expressed by splicing while ensuring accordance of the reading frame. More specifically, expression vector (v) is structured such that the fusion protein of the active XBP1 protein and the first reporter protein is expressed only by the splicing by IRE1.

The first reporter protein is not particularly limited insofar as its expression can be confirmed. A protein having a fluorescence activity is preferable in terms of easy confirmation in vivo. Examples of proteins having a fluorescence activity include luciferase, green fluorescent protein (GFP), and mutants thereof. Examples of luciferase include firefly luciferase, and Renilla luciferase. Examples of green fluorescent proteins and mutants thereof include *Aequorea victoria* green fluorescent protein, EGFP (enhanced green fluorescent protein), YFP (yellow fluorescent protein), BFP (blue fluorescent protein), and RFP (red fluorescent protein). They are all commercially available, and can be easily obtained.

#### Gene for UMAI System

The expression vector (w) has a fusion gene of ATF4 gene and the gene encoding the second reporter protein. The gene encoding the second reporter protein is located in the downstream of the true translation start point of the ATF4 gene.

Under endoplasmic reticulum stress, PERK is activated, and eIF-2 $\alpha$  is phosphorylated. As a result, the function of eIF-2 $\alpha$  decreases, thereby promoting the translation from the true translation start point, which is located undermost in the stream, among the multiple translation start points in mRNA of ATF4. Examples of known cDNA sequences of ATF4 include ATF4 of human, mice, and Aplysia. They are published in the EST database as HSU03712, NM\_009716, and ACU40851, respectively. In the present invention, cDNA of human ATF4 (hereinafter referred to as "Sequence 3"), NCBI registration No. BC011994, is used as cDNA of ATF4. After the transcription by mRNA, under a normal condition, i.e., when eIF-2 $\alpha$  normally functions, cDNA of ATF4 is translated from the false multiple upstream translation start point. More specifically, the positions 4 to 9, 67 to 78, and 166 to 345 of Sequence 3 are translated. On the other hand, upon activation of PERK, positions 263 to 1318 in Sequence 3, which is the true translation start point of mRNA of ATF4, are translated.

The gene encoding the second reporter protein is located in the downstream of the true translation start point of ATF4 gene. For example, regarding cDNA of human ATF4 having NCBI registration No. HSU03712, the gene encoding the second reporter protein is located downstream of position 263 of Sequence 3, more specifically, downstream of the true translation initiation codon (positions 263 to 265 in SEQ ID NO: 5). Accordingly, only when the translation starts from the true translation start point in response to the activation of PERK is the second reporter protein expressed.

As with the first reporter protein, the second reporter protein is not particularly limited insofar as its expression can be confirmed. A protein having a fluorescence activity is preferably used as the second reporter protein in terms of easy confirmation in vivo. However, the second reporter protein must be a different protein from the first reporter protein so that its expression can be easily distinguished from the expression of the first reporter protein. Examples of the combination of the first reporter protein and the second reporter protein include a combination of a firefly luciferase and a Renilla luciferase, and a combination of EGFP and RFP.

With transgenic cells containing the expression vectors (v) and (w), the cells are cultured under appropriate conditions, for example, in an appropriate culture medium generally selected by a person skilled in the art. Then, the cells are brought into contact with a drug to be screened. The step of bringing the cells into contact with a drug may be performed by, for example, adding the drug in the culture medium, injecting the drug into the cells, or the like. After keeping the cells in contact with the drug for a predetermined duration, the expressions of the first reporter protein and the second reporter protein are measured. Usually, the expressions are

measured by measuring the activities of the expressed proteins. For example, when the reporter protein is a fluorescent protein, the fluorescence intensity of the cells is measured.

If only the first reporter protein shows an increase in activity, it indicates that only IRE1 $\alpha$  pathway is activated. Conversely, if only the second reporter protein shows an increase in activity, it indicates that only PERK pathway is activated. Further, if the increase in activity was observed in both the first and second reporter proteins, it indicates that both IRE1 $\alpha$  pathway and PERK pathway are activated. If the increase in activity was not observed in either the first or second reporter protein, it indicates that neither IRE1 $\alpha$  pathway nor PERK pathway are activated.

The combination of the screen method of the present invention and a hitherto-known screening method is not particularly limited. The following combinations are possible.

Instead of the screening transformant used in the example described in “(5) Transformant of the Present Invention,” a transformant (hereinafter referred to as “transformant for 3-pathway detection”) obtained by further adding the expression vectors (v) and (w) to the above transformant may be used. Here, the fluorescent protein and the first and second reporter proteins are selected in view of secure differentiation between the fluorescence intensity of the fluorescent protein used for the present screening method, the fluorescence intensity or activity of the first reporter protein, and the fluorescence intensity or activity of the second reporter protein. By bringing the transformant for 3-pathway detection into contact with an endoplasmic reticulum stressor candidate substance, and then comparing the test cells with the control cells in terms of the fluorescence intensity of the fluorescent protein and the fluorescence intensity or activity of the reporter proteins, it is possible to determine which of the aforementioned endoplasmic reticulum stressors (o) to (u) corresponds to the candidate substance.

The present screening method enables discovery of a substance that causes endoplasmic reticulum stress, and is thus useful for research regarding the mechanism of endoplasmic reticulum stress; or research regarding the treatment of diabetes or neurodegenerative disorders caused by endoplasmic reticulum stress.

#### (6-2) a Method for Screening Endoplasmic Reticulum Stress Inhibitor

A method for screening an endoplasmic reticulum stress inhibitor includes a step of (d) bringing an endoplasmic reticulum stressor and a test substance with the screening transformant used in the example described in “(5) Transformant of the Present Invention”; a step of (e) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance; and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant that is not in contact with the test substance, but in contact with the endoplasmic reticulum stressor; and a step of (f) selecting the test substance as an endoplasmic reticulum stress inhibitor when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance is higher than the fluorescence intensity of the control transformant.

The endoplasmic reticulum stressor is not particularly limited insofar as it is a substance that causes endoplasmic reticulum stress. Examples of such substances include tunicamycin, thapsigargin, and DTT (dithiothreitol). Further, the endoplasmic reticulum stressor screened by the above method for screening endoplasmic reticulum stressor may also be used.

The type of the test substance is not particularly limited. Examples of the test substances include proteins, peptides, non-peptidic compounds (nucleotides, amines, saccharides, lipids, etc.), organic low-molecular-weight compounds, inorganic low-molecular-weight compounds, fermentation products, cell extracts, plant extracts, and animal tissue extracts.

The step of bringing the test substance into contact with the cells may be performed under conditions (in terms of temperature, pH, components of culture medium) in which the cells are kept alive and the fusion protein of the nonfluorescent peptide domain 1 derived from a fluorescent protein and the ATF6 protein domain, and the protein containing a non-fluorescent peptide domain 2 derived from a fluorescent protein can be expressed from the introduced transgenic vector. The concentration of the endoplasmic reticulum stressor candidate substance to be brought into contact with the cells varies depending on the type of the substance. For example, the concentration is about 0.001 to 100  $\mu$ g/ml.

Further, screening of an organ-specific substance for suppressing endoplasmic reticulum stress becomes possible by using the transformant of the present invention derived from the target organ. For example, screening of a liver-specific substance for suppressing endoplasmic reticulum stress may be performed using the transformant of the present invention derived from hepatic cells.

The present screening method enables screening of a substance for suppressing endoplasmic reticulum stress, and thus is useful for research regarding the treatment of diabetes or neurodegenerative disorders caused by endoplasmic reticulum stress.

#### (6-3) A Method for Screening Antidiabetic Drug Candidate

A method for screening an antidiabetic drug candidate includes a step of (g) bringing an endoplasmic reticulum stressor and a test substance with the antidiabetic drug candidate screening transformant used in the example described in “(5) Transformant of the Present Invention”; a step of (h) measuring the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance, and comparing the measured fluorescence intensity with the fluorescence intensity of a control transformant that is not in contact with the test substance, but that is in contact with the endoplasmic reticulum stressor; and a step of (i) selecting the test substance as an antidiabetic drug candidate when the fluorescence intensity of the transformant in contact with the endoplasmic reticulum stressor and the test substance is higher than the fluorescence intensity of the control transformant.

The endoplasmic reticulum stressor is not particularly limited insofar as it is a substance that causes endoplasmic reticulum stress. Examples of such substances include tunicamycin, thapsigargin, and DTT. Further, the endoplasmic reticulum stressor screened by the above method for screening endoplasmic reticulum stressor may also be used.

The type of the test substance is not particularly limited. Examples of the test substances include proteins, peptides, non-peptidic compounds (nucleotides, amines, saccharides, lipids, etc.), organic low-molecular-weight compounds, inorganic low-molecular-weight compounds, fermentation products, cell extracts, plant extracts, and animal tissue extracts.

The step of bringing the test substance into contact with the cells may be performed under conditions (in terms of temperature, pH, components of culture medium) in which the cells are kept alive and the fusion protein of the nonfluorescent peptide domain 1 derived from a fluorescent protein and the ATF6 protein domain, and the protein containing a non-fluorescent peptide domain 2 derived from a fluorescent protein can be expressed from the introduced transgenic vector.



The concentration of the endoplasmic reticulum stressor candidate substance to be brought into contact with the cells varies depending on the type of the substance. For example, the concentration is about 0.001 to 100 µg/ml.

The antidiabetic drug candidate selected by the present screening method may further be subjected to a pharmacological effectiveness test or pharmacological safety test using pathological animal models, thereby producing a further useful antidiabetic drug.

## EXAMPLES

The present invention is more specifically explained below with reference to Examples. However, the present invention is not limited to these examples, etc.

An EGFPs-ATF6d expression vector and an EGFP expression vector were produced using a green fluorescent protein GFP as a reporter protein. An ATF6 activity reporter system having the two vectors was introduced into the following cell strains. As shown in FIG. 4, the EGFPs-ATF6d expression vector was produced by inserting a green fluorescent protein cDNA fragment (portion 1 (SEQ ID NO: 18) in FIG. 4: a DNA fragment encoding an amino acid region of the 216th to 231st (amino acid number) amino acids in SEQ ID NO: 1), a spacer (portion 2 (SEQ ID NO: 19) in FIG. 4: a DNA fragment encoding an amino acid sequence GGGSGGGS (SEQ ID NO: 10)), a 3XFLAG tag (portion 3 (SEQ ID NO: 20) in FIG. 4: a DNA fragment encoding an amino acid sequence DYKDDHDGDYKDDHDYKDDDDK (SEQ ID NO: 11)), a nuclear localization signal (portion 4 (SEQ ID NO: 21) in FIG. 4: a DNA fragment encoding an amino acid sequence DPKKKRKx3 (SEQ ID NO: 12)), a PEST sequence (portion 5 (SEQ ID NO: 22) in FIG. 3: a DNA fragment encoding an amino acid sequence SHGFPPEVE-EQDDGTLPMSCAQESGMDRHPAACASARINV (SEQ ID NO: 9)), and a partial cDNA fragment of mice ATF6α (portion 6 (SEQ ID NO: 23) in FIG. 4: a DNA fragment encoding an amino acid region of the 361st to 656th amino acids in SEQ ID NO: 2) into pEGFP-Puro. As shown in FIG. 5, the EGFP expression vector was produced by inserting a nuclear localization signal (portion 7 (SEQ ID NO: 25) in FIG. 5: a DNA fragment encoding an amino acid sequence DPKKKRKx3 (SEQ ID NO: 12)) and a green fluorescent protein cDNA fragment (portion 8 (SEQ ID NO: 26) in FIG. 5: an amino acid region of the 1st to 215th amino acids in SEQ ID NO: 1) into pEGFP-N1. pEGFP-Puro and pEGFP-N1 are capable of high expression of genes inserted into the downstream of the cytomegalovirus promoter and the enhancer in mammal cells.

### 1. Production of EGFPs-ATF6d Expression Vector

The production of the EGFPs-ATF6d expression vector was performed in the following three steps.

Step 1: Through artificial gene synthesis, four types of double strand DNA individually encoding a green fluorescent protein cDNA fragment, a spacer, a 3XFLAG tag, and a nuclear localization signal (portions 1, 2, 3, and 4 in FIG. 4) were synthesized and inserted into a pEGFP-Puro expression vector, thereby producing an EGFPs expression vector.

Step 2: A mouse ATF6α partial cDNA fragment (portions 6 in FIG. 4) obtained by PCR of kpn.mATF6d.SP1 (sequence: 5'-CTAGGGTACCCCAAAGCGAAGAGCTGTCTG-3' (SEQ ID NO: 13)) and not.mATF6d.AP1 (sequence: 5'-TTTTTTCCTTGCGGCCGCCTACTGCAAC-GACTCAGGGA-3' (SEQ ID NO: 14)) from mouse cDNA was inserted into a EGFPs expression vector, thereby producing a EGFPs-ATF6d-PEST(-) expression vector.

Step 3: A mouse ODC PEST sequence (portion 5 in FIG. 4) obtained by PCR of xho.PEST.SP1 (sequence: 5'-CTAGCTCGAGAGCCATGGCTTCCCGCCGGC-3' (SEQ ID NO: 15)) and kpn.PEST.AP1 (sequence: 5'-CTAGGGTACCCACATTGATCCTAGCAGAAG-3' (SEQ ID NO: 16)) from mouse cDNA was inserted into an EGFPs-ATF6d-PEST(-) expression vector, thereby producing an EGFPs-ATF6d expression vector.

The EGFPs expression vector, the EGFPs-ATF6d-PEST(-) expression vector, and the EGFPs-ATF6d expression vector also have a pEGFP-Puro derived puromycin drug resistance gene.

### 2. Production of EGFP Expression Vector

Through artificial gene synthesis, two double-strand DNA individually encoding a nuclear localization signal and a green fluorescent protein (portions 7 and 8 in FIG. 5) were synthesized and inserted into a pEGFP-N1 expression vector, thereby producing a EGFP expression vector. The EGFP expression vector also has a neomycin drug resistance gene.

### 3. Cell Culture

Unless otherwise specified, HEK293 cells (ATCC No.: CRL-1573), MIN6 cells (pancreatic β-cells reported by Miyazaki J et al., *Endocrinology* 127:126-132(1990)), HepG2 cells (ATCC No.: HB-8065), 3T3-L1 cells (ATCC No.: CL-173), L6 cells (ATCC No.: CRL-1458), and the cells introduced in the ATF6 activity reporter system (described later) were cultured under a condition of 37° C. and 5% CO<sub>2</sub> using a culture medium obtained by adding 10% fetal bovine serum to DMEM.

### 4. Preparation of Cells Containing ATF6 Activity Reporter System

The EGFPs-ATF6d expression vector and the EGFP expression vector were introduced into HEK293 cells using a polyethylene imine method at an efficiency of not less than 90%. Through an electroporation method using NEON (electroporation device) (Invitrogen), the EGFPs-ATF6d expression vector and the EGFP expression vector were introduced into MIN6 cells, HepG2 cells, 3T3-L1 cells, and L6 cells at an efficiency of not less than 80%, 60%, 90%, and 70%, respectively.

### 5. Confirmation of ATF6 Activity Reporter System

In order to confirm that the ATF6 activity reporter system functions in an endoplasmic reticulum stress-dependent manner, the EGFPs-ATF6d expression vector and the EGFP expression vector were coexpressed or individually expressed in HEK293 cells. The fluorescence signal of the cells was observed with an inverted fluorescence microscope DMI6000B (Leica); and a fluorescence signal was captured by a Rolera-XR CCD camera (QImaging) and analyzed using "Image-Pro Plus" software (Media Cybernetics; image analysis software).

As shown in FIG. 6, under general culture conditions, no green fluorescence was observed in the cells in which the EGFPs-ATF6d expression vector and the EGFP expression vector were individually expressed. In the cells in which the EGFPs-ATF6d expression vector and the EGFP expression vector were coexpressed, green fluorescence was slightly observed. The cells were stimulated with 0.2 µg/ml tunicamycin, which is an endoplasmic reticulum stress inducer, and observed 6 hours after the stimulation. As a result, no green fluorescence was observed in the cells in which the EGFPs-ATF6d expression vector and the EGFP expression vector were individually expressed, and significant green fluorescence was observed in the cells in which the EGFPs-ATF6d expression vector and the EGFP expression vector were coexpressed.

This showed that the divided green fluorescent proteins do not individually yield fluorescence, and that the ATF6 activity reporter system functions in response to endoplasmic reticulum stress.

#### 6. Confirmation of Endoplasmic Reticulum Stress Specificity of Atf6 Activity Reporter System

It is important that ATF6 activity reporter system is capable of detecting ATF6 activation in an endoplasmic reticulum stress-specific manner. Therefore, HEK293 cells in which the EGFPs-ATF6d expression vector and the EGFP expression vector are coexpressed are stimulated by etoposide, which is a DNA replication inhibitor; thapsigargin, which is an endoplasmic reticulum stress inducer; and DTT, which is an endoplasmic reticulum stress inducer, in an amount of 100  $\mu$ M, 0.2  $\mu$ M, and 1 mM, respectively; and the presence of fluorescence was observed. With Hoechst33258 staining, it was confirmed that the induced stresses were all severe enough to cause cell death after 36 hours.

However, as shown in FIG. 7, no green fluorescence was observed in the cells stimulated by etoposide, which is irrelevant to endoplasmic reticulum stress; and significant green fluorescence was observed in the cells stimulated by thapsigargin or DTT, which are endoplasmic reticulum stress inducers.

This showed that the ATF6 activity reporter system is capable of detection of ATF6 activation in an endoplasmic reticulum stress-specific manner.

#### 7. Confirmation of Specificity of Endoplasmic Reticulum Stress Response Pathway of ATF6 Activity Reporter System

The endoplasmic reticulum stress response is known to be controlled by three individual pathways. It is important that the ATF6 activity reporter system enables detection of ATF6 activation with no influence of other pathways, such as Ire1 pathway or PERK pathway. In this connection, the EGFPs-ATF6d expression vector and the EGFP expression vector were coexpressed in mouse fibroblasts modified by deleting Ire1 $\alpha$  gene or PERK gene. The cells were observed 6 hours after stimulation with 0.2  $\mu$ g/ml tunicamycin, which is an endoplasmic reticulum stress inducer.

As shown in FIG. 8, significant green fluorescence was observed both in the fibroblast modified by Ire1 $\alpha$  gene deletion, and in the fibroblast modified by PERK gene deletion due to the stimulation with tunicamycin.

This showed that the ATF6 activity reporter system is capable of detection of ATF6 activation with no influence of Ire1 pathway or PERK pathway.

#### 8. Confirmation of Importance of Spacer in Egfps-Atf6d Expression Vector

To obtain a high fluorescence signal, efficient restructuring of the divided fluorescence green proteins is necessary. Thus, it is important to add an appropriate spacer that does not hinder the association of the divided fluorescence green proteins. To find an appropriate length of the spacer, as shown in FIG. 9, two double-strand DNA were produced through artificial gene synthesis, and inserted into a pEGFPs-ATF6d expression vector so as to produce a pEGFPs-ATF6d-SP1 expression vector and a pEGFPs-ATF6d-SP3 expression vector that respectively have a spacer GGGS (SEQ ID NO: 5) and a spacer GGGSGGGSGGGGS (SEQ ID NO: 6). HEK293 cells in which an EGFP expression vector and either a pEGFPs-ATF6d-SP1 expression vector (spacer GGGS (SEQ ID NO: 5)), an EGFPs-ATF6d expression vector (spacer GGGSGGGGS SEQ ID NO: 10)), or a pEGFPs-ATF6d-SP3 expression vector (spacer GGGSGGGSGGGGS (SEQ ID NO: 6)) were coexpressed were stimulated with 0.2  $\mu$ g/ml tunicamycin, which is an endoplasmic reticulum stress inducer. Six hours after the stimulation, the cells were observed.

As shown in FIG. 10, the green fluorescence was more significantly observed in the cells in which the spacer GGGSGGGGS (SEQ ID NO: 10) or the spacer

GGGSGGGSGGGSGGGGS (SEQ ID NO: 6), both longer than the spacer GGGS (SEQ ID NO: 5), was expressed.

This confirmed the importance of the length of the spacer in the present system.

#### 9. Confirmation of Importance of PEST Sequence in EGFPs-ATF6d Expression Vector

The endoplasmic reticulum stress response is indispensable for the homeostasis of endoplasmic reticulum. The endoplasmic reticulum stress response is induced not only under a pathological condition, but also under a physiological condition. In the cells cultured under a general culture condition, weak endoplasmic reticulum stress response is usually induced. Accordingly, in the cells in which the ATF6 activity reporter system is expressed, the endoplasmic reticulum stress is assumed to cause accumulation of green fluorescent protein serving as a reporter, thereby producing a high background signal. In this regard, the cells in which a EGFP expression vector and either an EGFPs-ATF6d expression vector for expressing a mouse ODC PEST sequence that promotes degradation of green fluorescent protein, or an EGFPs-ATF6d-PEST(-) expression vector that does not have a mouse ODC PEST sequence are coexpressed were stimulated with 2  $\mu$ g/ml tunicamycin, which is an endoplasmic reticulum stress inducer. The cells were observed before the stimulation, and 6 hour after the stimulation.

As shown in FIG. 11, green fluorescence was significantly weakened by a PEST sequence in the cells cultured under a general culture condition. Under the stimulation with tunicamycin, although the induction of green fluorescence was slightly decreased by the PEST sequence, the rate of increase in green fluorescence luminance by the stimulation was increased by the PEST sequence.

This confirmed the importance of the PEST sequence in the present system.

#### 10. Confirmation of Detection of Difference in Organ-Specific Endoplasmic Reticulum Stress Response Signal Using ATF6 Activity Reporter System

The endoplasmic reticulum stress response is controlled by the three pathways, namely, Ire1 pathway, PERK pathway, and ATF6 pathway. Apart from the homeostasis of endoplasmic reticulum, they are also individually involved in control of organ-specific metabolism. Detection of the three endoplasmic reticulum stress response pathways is considered important to discover a drug targeting organ-specific endoplasmic reticulum stress response with fewer side effects. In this regard, as shown in FIG. 12, an Ire1 activation reporter expression vector, disclosed in Nat. Med. (2004) 10 98-102, for measuring Ire1 pathway by XBP1 splicing, and a PERK activation reporter expression vector, disclosed in J Cell Biol. (2004) 167 27-33, for measuring PERK pathway by ATF4 translation were produced. An EGFPs-ATF6d expression vector, an EGFP expression vector, the Ire1 activation reporter expression vector, and the PERK activation reporter expression vector were expressed in pancreatic  $\beta$ -cell strain MIN6 cells, hepatic cell strain HepG2 cells, adipose cell strain 3T3-L1 cells, and skeletal muscle cell strain L6 cells, respectively. The cells were observed 6 hours after the stimulation with 0.2  $\mu$ g/ml tunicamycin, which is an endoplasmic reticulum stress inducer. FIG. 13 shows an image of fluorescence in the cells observed with an inverted fluorescence microscope DMI6000B (Leica). Further, FIG. 14 shows the results of determination of fluorescence intensity of the cells measured by "Image-Pro Plus" (Media Cybernetics) software using a fluorescence microscope cell image captured by a CCD camera Rolera-XR (QImaging).

As shown in FIG. 13, the endoplasmic reticulum stress response signal varies in each cell group derived from a different organ, even under the same stress conditions.

Further, as shown in FIG. 14, the activation of IRE1 pathway by tunicamycin is relatively high in hepatic cell strain

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HepG2 cells, pancreatic  $\beta$ -cell strain MIN6 cells and skeletal muscle cell strain L6 cells, and relatively low in adipose cell strain 3T3-L1 cells. Further, the intensity of activation of ATF6 pathway by tunicamycin is highest in hepatic cell strain HepG2 cells, followed by pancreatic  $\beta$ -cell strain MIN6 cells, skeletal muscle cell strain L6 cells, and adipose cell strain 3T3-L1 cells in descending order. Further, the degree of the activation of PERK pathway by tunicamycin is highest in hepatic cell strain HepG2 cells (pancreatic  $\beta$ -cell strain MIN6 cells and skeletal muscle cell strain L6 cells), followed by adipose cell strain 3T3-L1 cells.

This showed that the combination of the present system with a hitherto-known technique enables confirmation of the organ-specific difference in signal intensity from the three endoplasmic reticulum stress response pathways. Further, it was also confirmed that it is possible to screen an endoplasmic reticulum stressor that activates only the ATF6 pathway among three pathways (pathways mediated by IRE1 $\alpha$ , PERK, and ATF6), or an endoplasmic reticulum stressor that activates at least one pathway selected from the group consisting of the ATF6 pathway, IRE1 $\alpha$  pathway, and PERK pathway.

#### 11. Inhibition of Insulin Secretion in Pancreatic $\beta$ -Cells

A control solution (DMSO), a thapsigargin solution (thapsigargin/DMSO solution), or a DTT solution (DTT/DMSO solution) was added to a culture solution (DMEM containing 10% fetal bovine serum) in which pancreatic  $\beta$ -cell MIN6 cells are cultured, and the culture solution was replaced with a general culture solution (DMEM containing 10% fetal bovine serum) after 30 minutes. Then, the culture was continued for 36 hours. The thapsigargin solution was added so that the thapsigargin concentration in the culture solution became 0.2  $\mu$ M, and the DTT solution was added so that the DTT concentration in the culture solution became 1 M. Thereafter, the culture solution was replaced with a KREBS buffer solution containing 3 mM or 20 mM glucose, and the culture was continued for 1 hours. The concentration of insulin secreted in the culture solution was measured according to the ELISA method. FIG. 15 shows the results.

As shown in FIG. 15, by the addition of thapsigargin or DTT, which is an endoplasmic reticulum stress inducer, insulin secretion was suppressed.

#### 12. Comparison of Detection Sensitivity Between ATF6 Activity Reporter System and Hitherto-Known Method (Western Blotting)

A comparison of detection sensitivity in the detection of ATF6 pathway activation between the ATF6 activity reporter system and a hitherto-known method (western blotting) was conducted.

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The detection sensitivity of the ATF6 activity reporter system was measured as follows. Adipose cell strain 3T3-L1 cells obtained in the same manner as in "4. Preparation of Cells containing ATF6 Activity Reporter System" were stimulated using a known differentiation-inducing stimulation method (exposure to insulin, dexamethasone, and 3-isobutyl-1-methylxanthine). 14 days after the stimulation, a test compound (one of Compounds 1 to 10) was added as an endoplasmic reticulum stressor candidate substance, and a stimulator (palmitic acid) for inducing endoplasmic reticulum stress or the like was added after 6 hours so that the final concentration became 400  $\mu$ M. After another 16 hours, the cell image was obtained by an inverted fluorescence microscope DMI6000B (Leica), and the intensity of fluorescence emitted from the cells was measured using "Image-Pro Plus" (Media Cybernetics) image analysis software.

The detection sensitivity in the hitherto-known method (western blotting) was measured as follows. Adipose cell strain 3T3-L1 cells were stimulated using a known differentiation-inducing stimulation method (exposure to insulin, dexamethasone, and 3-isobutyl-1-methylxanthine). 14 days after the stimulation, a test compound (one of Compounds 1 to 10) was added, and a stimulator for inducing endoplasmic reticulum stress or the like was added after 6 hours. After another 16 hours, the cells were collected. A cell extract was prepared from the obtained cells, and the expression amount of ATF6 $\alpha$  protein was detected through western blotting using anti-ATF6  $\alpha$  antibody mouse monoclonal (BioAcademia 73-505). The detected signal intensity was measured using "Image-Pro Plus" (Media Cybernetics) software.

FIG. 16 shows the results. The fluorescence intensity or signal intensity in the vertical axis is denoted by a value that is determined by assuming that the intensity in the control (test compound is not added) is 1. More specifically, 1 or more intensity in the vertical axis indicates activation of ATF6 pathway by the test compound. The horizontal axis shows the numbers (1-10) of the test compounds.

Activation of ATF6 pathway was not observed by the addition of any of the test compounds 1 to 10 in the hitherto-known method. In contrast, in the present method, activation of ATF6 pathway was observed when the test compounds 4, 5, 6, 7, 8, or 10 was added (1.2 times the control).

The results showed that the present method is capable of detecting a very small amount of activation of ATF6 pathway, which is not detectable by the hitherto-known method. More specifically, the present method ensures a detection sensitivity significantly superior to the detection sensitivity of the hitherto-known method. [Sequence Table]

## SEQUENCE LISTING

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<210> SEQ ID NO 1

<211> LENGTH: 231

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: EGFP amino acid sequence

<400> SEQUENCE: 1

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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Arg Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Ile Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

-continued

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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
 50 55 60  
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
 65 70 75 80  
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
 85 90 95  
 Arg Thr Ile Ser Phe Lys Asp Asp Gly Lys Tyr Lys Thr Arg Ala Val  
 100 105 110  
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
 115 120 125  
 Thr Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
 130 135 140  
 Asn Phe Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn  
 145 150 155 160  
 Gly Ile Lys Ala Asn Phe Thr Val Arg His Asn Val Glu Asp Gly Ser  
 165 170 175  
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
 180 185 190  
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Thr Val Leu  
 195 200 205  
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&lt;213&gt; ORGANISM: Mus musculus

&lt;400&gt; SEQUENCE: 2

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 Asp Val His Phe Asp Ala Ala His Glu Ala Tyr Glu Asn Asn Phe Asp  
 35 40 45  
 His Leu Asn Phe Asp Leu Asp Leu Met Pro Trp Glu Ser Asp Leu Trp  
 50 55 60  
 Ser Pro Gly Ser His Phe Cys Ser Asp Met Lys Ala Glu Pro Gln Pro  
 65 70 75 80  
 Leu Ser Pro Ala Ser Ser Ser Cys Ser Ile Ser Ser Pro Arg Ser Thr  
 85 90 95  
 Asp Ser Cys Ser Ser Thr Gln His Val Pro Glu Glu Leu Asp Leu Leu  
 100 105 110  
 Ser Ser Ser Gln Ser Pro Leu Ser Leu Tyr Gly Asp Ser Cys Asn Ser  
 115 120 125  
 Pro Ser Ser Val Glu Pro Leu Lys Glu Glu Lys Pro Val Thr Gly Pro  
 130 135 140  
 Gly Asn Lys Thr Glu His Gly Leu Thr Pro Lys Lys Lys Ile Gln Met  
 145 150 155 160  
 Ser Ser Lys Pro Ser Val Gln Pro Lys Pro Leu Leu Leu Pro Ala Ala  
 165 170 175  
 Pro Lys Thr Gln Thr Asn Ala Ser Val Pro Ala Lys Ala Ile Ile Ile  
 180 185 190

-continued

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Gln Thr	Leu Pro	Ala Leu	Met Pro	Leu Ala	Lys Gln	Gln Ser	Ile Ile		
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Ser Ile	Gln Pro	Ala Pro	Thr Lys	Gly Gln	Thr Val	Leu Leu	Ser Gln		
	210		215			220			
Pro Thr	Val Val	Gln Leu	Gln Ser	Pro Ala	Val Leu	Ser Ser	Ala Gln		
	225		230			235			240
Pro Val	Leu Ala	Val Thr	Gly Gly	Ala Ala	Gln Leu	Pro Asn	His Val		
		245			250		255		
Val Asn	Val Leu	Pro Ala	Pro Val	Val Ser	Ser Pro	Val Asn	Gly Lys		
	260			265		270			
Leu Ser	Val Thr	Lys Pro	Val Leu	Gln Ser	Ala Thr	Arg Ser	Met Gly		
	275			280		285			
Ser Asp	Ile Ala	Val Leu	Arg Arg	Gln Gln	Arg Met	Ile Lys	Asn Arg		
	290		295		300				
Glu Ser	Ala Cys	Gln Ser	Arg Lys	Lys Lys	Lys Glu	Tyr Met	Leu Gly		
	305		310		315		320		
Leu Glu	Ala Arg	Leu Lys	Ala Ala	Leu Ser	Glu Asn	Glu Gln	Leu Lys		
		325			330		335		
Lys Glu	Asn Gly	Ser Leu	Lys Arg	Gln Leu	Asp Glu	Val Val	Ser Glu		
	340			345		350			
Asn Gln	Arg Leu	Lys Val	Pro Ser	Pro Lys	Arg Arg	Ala Val	Cys Val		
	355			360		365			
Met Ile	Val Leu	Ala Phe	Ile Met	Leu Asn	Tyr Gly	Pro Met	Ser Met		
	370		375		380				
Leu Glu	Gln Glu	Ser Arg	Arg Val	Lys Pro	Ser Val	Ser Pro	Ala Asn		
	385		390		395		400		
Gln Arg	Arg His	Leu Leu	Glu Phe	Ser Ala	Lys Glu	Val Lys	Asp Thr		
		405			410		415		
Ser Asp	Gly Asp	Asn Gln	Lys Asp	Ser Tyr	Ser Tyr	Asp His	Ser Val		
	420			425		430			
Ser Asn	Asp Lys	Ala Leu	Met Val	Leu Ser	Glu Glu	Pro Leu	Leu Tyr		
	435			440		445			
Met Pro	Pro Pro	Pro Cys	Gln Pro	Leu Ile	Asn Thr	Thr Glu	Ser Leu		
	450		455			460			
Arg Leu	Asn His	Glu Leu	Arg Gly	Trp Val	His Arg	His Glu	Val Glu		
	465		470		475		480		
Arg Thr	Lys Ser	Arg Arg	Met Thr	Asn Ser	Gln Gln	Lys Ala	Arg Ile		
		485			490		495		
Leu Gln	Gly Ala	Leu Glu	Gln Gly	Ser Asn	Ser Gln	Leu Met	Ala Val		
	500			505		510			
Gln Tyr	Thr Glu	Thr Thr	Ser Ile	Ser Arg	Asn Ser	Gly Ser	Glu Leu		
	515			520		525			
Gln Val	Tyr Tyr	Ala Ser	Pro Gly	Ser Tyr	Gln Gly	Phe Phe	Asp Ala		
	530		535			540			
Ile Arg	Arg Arg	Gly Asp	Thr Phe	Tyr Val	Val Ser	Phe Arg	Arg Asp		
	545		550		555		560		
His Leu	Leu Leu	Pro Ala	Thr Thr	His Asn	Lys Thr	Thr Arg	Pro Lys		
		565			570		575		
Met Ser	Ile Val	Leu Pro	Ala Ile	Asn Ile	Asn Asp	Asn Val	Ile Asn		
	580			585		590			
Gly Gln	Asp Tyr	Glu Val	Met Met	Gln Ile	Asp Cys	Gln Val	Met Asp		
	595			600		605			

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Thr Arg Ile Leu His Ile Lys Ser Ser Ser Val Pro Pro Tyr Leu Arg  
 610 615 620

Asp His Gln Arg Asn Gln Thr Ser Thr Phe Phe Gly Ser Pro Pro Thr  
 625 630 635 640

Thr Thr Glu Thr Thr His Val Val Ser Thr Ile Pro Glu Ser Leu Gln  
 645 650 655

<210> SEQ ID NO 3  
 <211> LENGTH: 670  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met Gly Glu Pro Ala Gly Val Ala Gly Thr Met Glu Ser Pro Phe Ser  
 1 5 10 15

Pro Gly Leu Phe His Arg Leu Asp Glu Asp Trp Asp Ser Ala Leu Phe  
 20 25 30

Ala Glu Leu Gly Tyr Phe Thr Asp Thr Asp Glu Leu Gln Leu Glu Ala  
 35 40 45

Ala Asn Glu Thr Tyr Glu Asn Asn Phe Asp Asn Leu Asp Phe Asp Leu  
 50 55 60

Asp Leu Met Pro Trp Glu Ser Asp Ile Trp Asp Ile Asn Asn Gln Ile  
 65 70 75 80

Cys Thr Val Lys Asp Ile Lys Ala Glu Pro Gln Pro Leu Ser Pro Ala  
 85 90 95

Ser Ser Ser Tyr Ser Val Ser Ser Pro Arg Ser Val Asp Ser Tyr Ser  
 100 105 110

Ser Thr Gln His Val Pro Glu Glu Leu Asp Leu Ser Ser Ser Gln  
 115 120 125

Met Ser Pro Leu Ser Leu Tyr Gly Glu Asn Ser Asn Ser Leu Ser Ser  
 130 135 140

Ala Glu Pro Leu Lys Glu Asp Lys Pro Val Thr Gly Pro Arg Asn Lys  
 145 150 155 160

Thr Glu Asn Gly Leu Thr Pro Lys Lys Lys Ile Gln Val Asn Ser Lys  
 165 170 175

Pro Ser Ile Gln Pro Lys Pro Leu Leu Leu Pro Ala Ala Pro Lys Thr  
 180 185 190

Gln Thr Asn Ser Ser Val Pro Ala Lys Thr Ile Ile Ile Gln Thr Val  
 195 200 205

Pro Thr Leu Met Pro Leu Ala Lys Gln Gln Pro Ile Ile Ser Leu Gln  
 210 215 220

Pro Ala Pro Thr Lys Gly Gln Thr Val Leu Leu Ser Gln Pro Thr Val  
 225 230 235 240

Val Gln Leu Gln Ala Pro Gly Val Leu Pro Ser Ala Gln Pro Val Leu  
 245 250 255

Ala Val Ala Gly Gly Val Thr Gln Leu Pro Asn His Val Val Asn Val  
 260 265 270

Val Pro Ala Pro Ser Ala Asn Ser Pro Val Asn Gly Lys Leu Ser Val  
 275 280 285

Thr Lys Pro Val Leu Gln Ser Thr Met Arg Asn Val Gly Ser Asp Ile  
 290 295 300

Ala Val Leu Arg Arg Gln Gln Arg Met Ile Lys Asn Arg Glu Ser Ala  
 305 310 315 320

Cys Gln Ser Arg Lys Lys Lys Lys Glu Tyr Met Leu Gly Leu Glu Ala  
 325 330 335

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Arg Leu Lys Ala Ala Leu Ser Glu Asn Glu Gln Leu Lys Lys Glu Asn
   340                               345                   350

Gly Thr Leu Lys Arg Gln Leu Asp Glu Val Val Ser Glu Asn Gln Arg
   355                               360                   365

Leu Lys Val Pro Ser Pro Lys Arg Arg Val Val Cys Val Met Ile Val
   370                               375                   380

Leu Ala Phe Ile Ile Leu Asn Tyr Gly Pro Met Ser Met Leu Glu Gln
   385                               390                   395                   400

Asp Ser Arg Arg Met Asn Pro Ser Val Ser Pro Ala Asn Gln Arg Arg
   405                               410                   415

His Leu Leu Gly Phe Ser Ala Lys Glu Ala Gln Asp Thr Ser Asp Gly
   420                               425                   430

Ile Ile Gln Lys Asn Ser Tyr Arg Tyr Asp His Ser Val Ser Asn Asp
   435                               440                   445

Lys Ala Leu Met Val Leu Thr Glu Glu Pro Leu Leu Tyr Ile Pro Pro
   450                               455                   460

Pro Pro Cys Gln Pro Leu Ile Asn Thr Thr Glu Ser Leu Arg Leu Asn
   465                               470                   475                   480

His Glu Leu Arg Gly Trp Val His Arg His Glu Val Glu Arg Thr Lys
   485                               490                   495

Ser Arg Arg Met Thr Asn Asn Gln Gln Lys Thr Arg Ile Leu Gln Gly
   500                               505                   510

Ala Leu Glu Gln Gly Ser Asn Ser Gln Leu Met Ala Val Gln Tyr Thr
   515                               520                   525

Glu Thr Thr Ser Ser Ile Ser Arg Asn Ser Gly Ser Glu Leu Gln Val
   530                               535                   540

Tyr Tyr Ala Ser Pro Arg Ser Tyr Gln Asp Phe Phe Glu Ala Ile Arg
   545                               550                   555                   560

Arg Arg Gly Asp Thr Phe Tyr Val Val Ser Phe Arg Arg Asp His Leu
   565                               570                   575

Leu Leu Pro Ala Thr Thr His Asn Lys Thr Thr Arg Pro Lys Met Ser
   580                               585                   590

Ile Val Leu Pro Ala Ile Asn Ile Asn Glu Asn Val Ile Asn Gly Gln
   595                               600                   605

Asp Tyr Glu Val Met Met Gln Ile Asp Cys Gln Val Met Asp Thr Arg
   610                               615                   620

Ile Leu His Ile Lys Ser Ser Ser Val Pro Pro Tyr Leu Arg Asp Gln
   625                               630                   635                   640

Gln Arg Asn Gln Thr Asn Thr Phe Phe Gly Ser Pro Pro Ala Ala Thr
   645                               650                   655

Glu Ala Thr His Val Val Ser Thr Ile Pro Glu Ser Leu Gln
   660                               665                   670

```

&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 238

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Aequorea victoria

&lt;400&gt; SEQUENCE: 4

```

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1           5           10           15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20           25           30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35           40           45

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Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
50						55					60				
Ala	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75					80
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
				100				105					110		
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
		130				135					140				
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
145					150					155					160
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
				165					170					175	
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro
			180					185					190		
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Val	Leu	Ser
			195				200					205			
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
	210					215					220				
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
225					230					235					

<210> SEQ ID NO 5  
 <211> LENGTH: 4  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: spacer

<400> SEQUENCE: 5

Gly Gly Gly Ser  
 1

<210> SEQ ID NO 6  
 <211> LENGTH: 12  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: spacer

<400> SEQUENCE: 6

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 1                      5                      10

<210> SEQ ID NO 7  
 <211> LENGTH: 6  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: the nuclear localization signal in the ATF6 protein

<400> SEQUENCE: 7

Arg Lys Lys Lys Lys Glu  
 1                      5



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```

<210> SEQ ID NO 8
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: the exogenous nuclear localization signal

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```

<400> SEQUENCE: 8

```

```

Asp Pro Lys Lys Lys Arg Lys Val
1          5

```

```

<210> SEQ ID NO 9
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: PEST sequences

```

```

<400> SEQUENCE: 9

```

```

Ser His Gly Phe Pro Pro Glu Val Glu Glu Gln Asp Asp Gly Thr Leu
1          5          10          15

```

```

Pro Met Ser Cys Ala Gln Glu Ser Gly Met Asp Arg His Pro Ala Ala
          20          25          30

```

```

Cys Ala Ser Ala Arg Ile Asn Val
          35          40

```

```

<210> SEQ ID NO 10
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: spacer

```

```

<400> SEQUENCE: 10

```

```

Gly Gly Gly Ser Gly Gly Gly Ser
1          5

```

```

<210> SEQ ID NO 11
<211> LENGTH: 22
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: 3XFLAG tag

```

```

<400> SEQUENCE: 11

```

```

Asp Tyr Lys Asp His Asp Gly Asp Tyr Lys Asp His Asp Ile Asp Tyr
1          5          10          15

```

```

Lys Asp Asp Asp Asp Lys
          20

```

```

<210> SEQ ID NO 12
<211> LENGTH: 24
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: nuclear localization signal

```

```

<400> SEQUENCE: 12

```

```

Asp Pro Lys Lys Lys Arg Lys Val Asp Pro Lys Lys Lys Arg Lys Val
1          5          10          15

```

```

Asp Pro Lys Lys Lys Arg Lys Val
          20

```

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```

<210> SEQ ID NO 13
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer (kpn.mATF6d.SP1)

<400> SEQUENCE: 13

ctagggtacc ccaaagcgaa gagctgtctg          30

<210> SEQ ID NO 14
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer (not.mATF6d.AP1)

<400> SEQUENCE: 14

ttttttcctt gcggccgcct actgcaacga ctcaggga          38

<210> SEQ ID NO 15
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer (xho.PEST.SP1)

<400> SEQUENCE: 15

ctagctcgag agccatggct tcccgcgcgc          30

<210> SEQ ID NO 16
<211> LENGTH: 30
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer (kpn.PEST.AP1)

<400> SEQUENCE: 16

ctagggtacc cacattgata ctagcagaag          30

<210> SEQ ID NO 17
<211> LENGTH: 1268
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence inserted in an EGFP-ATF6d
        expression vector

<400> SEQUENCE: 17

ctagccacca tgcgtgacca catggtcctt catgagtacg taaatgctgc tgggattaca          60
ggaggaggat cgggaggtgg cagcgactac aaagaccatg acggtgatta taaagatcat          120
gacatcgact acaaggatga cgatgacaag gatccaaaaa agaagagaaa ggtagatcca          180
aaaaagaaga gaaaggtaga tccaaaaaaag aagagaaaagg tactagcgct accggactca          240
gatctcgaga gccatggctt cccgccggcg gtggcggcgc aggatgatgg cacgtgccc          300
atgtcttctg cccaggagag cgggatggac cgtcaccctg cagcctgtgc ttctgctagg          360
atcaatgtgg gtaccccaaa gcgaagagct gtctgtgtga tgatagtatt agcatttata          420
atgctgaact atgggcccac gagcatgctg gagcaagaat cccgaagagt gaaacctagt          480
gtgagccctg ccaatcagag gaggcatttc ttggaatttt cagcaaaaga agttaagac          540
acatcagatg gtgacaacca gaaagacagt tacagctatg atcactctgt gtccaatgac          600
aaagctttaa tgggtgctaag tgaagagcca ttgctttata tgcctccacc tccatgtcaa          660

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```

ccccctgatta acacaacaga gtctctcagg ttgaaccatg aacttcgagg ctgggttcat 720
agacatgaag tggaaaggac caaatctaga agaatgacaa atagccaaca gaaagcccg 780
attctccagg gtgctctgga acagggtctt aattctcagc tgatggctgt ccagtacaca 840
gaaaccacta gcatcagtag gaattctggg agtgagctgc aagtgtatta cgctccct 900
ggaagttacc aaggtctctt tgacgccatc cgcaggaggg gagatacgtt ttacgttgtc 960
tcatttcgaa gggatcatct gctattacca gctaccacc acaacaagac cacaagacca 1020
aaaatgtcaa ttgtattacc agcaataaac ataatgata atgtgatcaa tgggcaggac 1080
tatgaagtaa tgatgcagat tgactgtcag gtgatggaca ccaggatcct ccacatcaaa 1140
agctctctcg tccccctta tctccgggat catcagcgga accaaaccag cacctcttt 1200
ggttcccctc caacaaccac agagacgacc catgttgtca gcaccatccc tgagtcgttg 1260
cagtaggc 1268

```

```

<210> SEQ ID NO 18
<211> LENGTH: 51
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 1 in Fig. 4: a DNA fragment encoding an
      amino acid region of the 216th to 231st (amino acid number) amino
      acids in SEQ ID NO: 1

<400> SEQUENCE: 18

atgcgtgacc acatgggtct tcatgagtac gtaaatgctg ctgggattac a 51

```

```

<210> SEQ ID NO 19
<211> LENGTH: 24
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 2 in Fig. 4: a DNA fragment encoding
      spacer

<400> SEQUENCE: 19

ggaggaggat ccggagggtgg cagc 24

```

```

<210> SEQ ID NO 20
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 3 in Fig. 4: a DNA fragment encoding
      FLAG tag

<400> SEQUENCE: 20

gactacaaag accatgacgg tgattataaa gatcatgaca tcgactacaa ggatgacgat 60
gacaag 66

```

```

<210> SEQ ID NO 21
<211> LENGTH: 72
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 4 in Fig. 4: a DNA fragment encoding a
      nuclear localization signal

<400> SEQUENCE: 21

gatccaaaaa agaagagaaa ggtagatcca aaaaagaaga gaaaggtaga tccaaaaaag 60
aagagaaagg ta 72

```

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```

<210> SEQ ID NO 22
<211> LENGTH: 120
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 5 in Fig. 3: a DNA fragment encoding a
      PEST sequence

<400> SEQUENCE: 22

agccatggct tccgcgcggc ggtggcggcg caggatgatg gcacgctgcc catgtcttgt      60
gccacaggaga gcgggatgga ccgtcacccct gcagcctgtg cttctgctag gatcaatgtg      120

<210> SEQ ID NO 23
<211> LENGTH: 891
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: portion 6 in Fig. 4: a DNA fragment encoding an
      amino acid region of the 361st to 656th amino acids in SEQ ID NO:
      2

<400> SEQUENCE: 23

ccaaagcgaa gagctgtctg tgtgatgata gtattagcat ttataatgct gaactatggg      60
cccatgagca tgctggagca agaatccga agagtgaac ctagtgtgag cctgccaat      120
cagaggaggc atctcttga attttcagca aaagaagtta aagacacatc agatggtgac      180
aaccagaaag acagttacag ctatgatcac tctgtgtcca atgacaaaagc ttaaatggtg      240
ctaagtgaag agccattgct ttatatgcct ccacctccat gtcaacccct gattaacaca      300
acagagtctc tcaggttgaa ccatgaactt cgaggctggg ttcatagaca tgaagtggaa      360
aggaccaaat ctagaagaat gacaaatagc caacagaaag cccgcattct ccagggtgct      420
ctggaacagg gctctaattc tcagctgatg gctgtocagt acacagaaac cactagcatc      480
agtaggaatt ctgggagtga gctgcaagtg tattacgcct cccctggaag ttaccaaggc      540
ttctttgacg ccacccgag gaggggagat acgttttacg ttgtotcatt tcgaagggat      600
catctgctat taccagctac caccacaaac aagaccacaa gacaaaaaat gtcaattgta      660
ttaccagcaa taaacataaa tgataatgtg atcaatgggc aggactatga agtaatgatg      720
cagattgact gtcagggtgat ggacaccagg atcctccaca tcaaaagctc ctcggttccc      780
ccttatctcc gggatcatca gcggaaccaa accagcacct tctttggttc ccctccaaca      840
accacagaga cgacccatgt ggtcagcacc atccctgagt cgttgcagta g      891

<210> SEQ ID NO 24
<211> LENGTH: 735
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: DNA sequence inserted in an EGFPL expression
      vector

<400> SEQUENCE: 24

ctagccacca tggatccaaa aaagaagaga aaggtagatc caaaaaagaa gagaaaggta      60
gatccaaaaa agaagagaaa ggtaatggtg agcaagggcg aggagctgtt caccgggggtg      120
gtgcccaccc tggtcgagct ggacggcgac gtaaacggcc acaagttcag cgtgagaggc      180
gaggcgaggg gcgatgccac catcggaag ctgacctga agttcatctg caccaccggc      240
aagctgcccg tgccctggcc caccctctg accaccctga cctacggcgt gcagtgttc      300
agccgctacc ccgaccacat gaagaggcac gacttcttca agtccgccat gccgaaggc      360

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tacgtccagg agcgcacccat ctctttcaag gacgacggca aatacaagac ccgcgccgta	420
gtgaagttcg agggcgacac cctggtgaac cgcacgcagc tgaagggcac tgacttcaag	480
gaggacggca acatcctggg gcacaagctg gagtacaact ttaacagcca caacgtctat	540
atcacggccg acaagcagaa gaacggcacc aaggctaact tcacagttcg ccacaacgtt	600
gaggacggca gcgtgcagct cgccgaccac taccagcaga acacccccat cggcgacggc	660
cccgtgctgc tgcccagaaa ccactacctg agcaccacaga ctgtcctgag caaagacccc	720
aacgagaagt aaagc	735

<210> SEQ ID NO 25  
 <211> LENGTH: 72  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: portion 7 in Fig. 5: a DNA fragment encoding a nuclear localization signal

<400> SEQUENCE: 25

gatccaaaaa agaagagaaa ggtagatcca aaaaagaaga gaaaggtaga tccaaaaaag	60
aagagaaagg ta	72

<210> SEQ ID NO 26  
 <211> LENGTH: 648  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: portion 8 in Fig. 5: an amino acid region of the 1st to 215th amino acids in SEQ ID NO: 1

<400> SEQUENCE: 26

atggtgagca agggcgagga gctgttcacc ggggtggtgc ccacccctggt cgagctggac	60
ggcgacgtaa acggccacaa gtccagcgtg agaggcgagg gcgagggcga tgccaccatc	120
ggcaagctga cctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca cctgaccta cggcgtgcag tgcttcagcc gctacccga ccacatgaag	240
aggcacgact tctcaagtc cgccatgcc gaaggctacg tccaggagcg caccatctct	300
ttcaaggacg acggcaaata caagaccgc gccgtagtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcactgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaacttta cagccacaac gtctatatca cggccgacaa gcagaagaac	480
ggcatcaagg ctaacttcac agttcgccac aacgttgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
tacctgagca ccagactgt cctgagcaaa gaccccaacg agaagtaa	648

<210> SEQ ID NO 27  
 <211> LENGTH: 197  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: a DNA sequence used for production of an EGFP-ATF6d expression vector in which the spacer is changed to GGGs

<400> SEQUENCE: 27

tacgtaaatg ctgctgggat tacaggaggt ggcagcgact acaaagacca tgacggtgat	60
tataaagatc atgacatcga ctacaaggat gacgatgaca aggatccaaa aaagaagaga	120

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aaggtagatc caaaaaagaa gagaaaggta gatccaaaaa agaagagaaa ggtactagcg      180
ctaccggact cagatct                                                    197

<210> SEQ ID NO 28
<211> LENGTH: 221
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: a DNA sequence used for production of an
EGFP-ATF6d expression vector in which the spacer is changed to
GGSGGGSGGGS

<400> SEQUENCE: 28

tacgtaaatg ctgctgggat tacaggagga ggatccggag gtggcagcgg aggtggcagc      60
gactacaaag accatgacgg tgattataaa gatcatgaca tcgactacaa ggatgacgat      120
gacaaggatc caaaaaagaa gagaaaggta gatccaaaaa agaagagaaa ggtagatcca      180
aaaaagaaga gaaaggtact agcgtaccg gactcagatc t                            221

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The invention claimed is:

1. A polynucleotide encoding an amino acid sequence having:

(1) a nonfluorescent peptide domain 1 of a fluorescent protein constituted of a nonfluorescent peptide domain 1 and a nonfluorescent peptide domain 2, characterized in that when nonfluorescent peptide domain 1 and nonfluorescent peptide domain 2 are associated, fluorescent activity is gained; and

(2) an ATF6 protein domain, wherein the polynucleotide has a region encoding (1) at the 5' end, a region encoding (2) at the 3' end, and a region encoding a PEST sequences between the region encoding (1) and the region encoding (2), wherein the polynucleotide does not encode the fluorescent protein, and

wherein the fluorescent protein is GFP, GFP mutants, or a GFP-like protein family member.

2. The polynucleotide according to claim 1, wherein the polynucleotide encodes an amino acid sequence in which the

nonfluorescent peptide domain 1 of said fluorescent protein and the PEST sequences are connected via a spacer having more than 6 amino acid residues.

3. A transgenic vector comprising the polynucleotide according to claim 1.

4. A transformed cultured cell comprising a transgenic vector according to claim 3.

5. The transformed cultured cell according to claim 4, further comprising a polynucleotide encoding an amino acid sequence having:

(3) the nonfluorescent peptide domain 2 of said fluorescent protein; and

(4) a nuclear localization signal peptide domain, in a state where a protein having the amino acid sequence having (3) and (4) can be expressed.

6. The transformed cultured cell according to claim 5, wherein the transformed cultured cell is a pancreatic  $\beta$ -cell.

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